SEARCH REQUEST FORM

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Serial
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Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

STAFF USE ONLY

Date completed: _____3/ 24_____

Searcher: _____S/L ... ... 773 25 26_____
7

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__✓__ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

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_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

__✓__ Other ...

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                GenCore version 5.1.6
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M nucleic - nucleic search, using sw model

un on:        March 21, 2004, 21:05:39 ; Search time 237 Seconds
                                         (without alignments)
                              12937.146 Million cell updates/sec

itle:          US-09-515-806a-1
erfect score:  5525
equence:       1 tcgcccacgcgtccgcacc........aatgcttcatatacctgca 5525

coring table:  IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

earched:       682709 seqs, 277475446 residues

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

Database :     Issued Patents NA:*
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             2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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             4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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             6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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otal number of hits satisfying chosen parameters: 1135418

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	244	4.4	244	4	US-09-016-434-785	Sequence 785, App
2	187.6	3.4	81001	4	US-09-750-580-1	Sequence 1, Appli
3	185.6	3.4	15297	4	US-09-817-180-3	Sequence 3, Appli
4	185.6	3.4	15297	4	US-10-003-285-3	Sequence 3, Appli
5	185.6	3.4	176373	3	US-09-128-155-17	Sequence 17, Appl
6	181.2	3.3	44848	4	US-09-435-739-42	Sequence 42, Appl
7	179	3.2	59065	4	US-09-813-817-3	Sequence 3, Appli
8	179	3.2	59065	4	US-09-978-197-3	Sequence 3, Appli
9	177.6	3.2	3166	4	US-09-341-587-8	Sequence 8, Appli
10	177.2	3.2	4079	4	US-09-016-434-1449	Sequence 1449, Ap
11	176.8	3.2	81001	4	US-09-750-580-1	Sequence 1, Appli
12	176.2	3.2	6769	1	US-08-480-784-20	Sequence 20, Appl
13	176.2	3.2	6769	1	US-08-483-553-20	Sequence 20, Appl
14	176.2	3.2	6769	1	US-08-487-002-20	Sequence 20, Appl
15	176.2	3.2	6769	1	US-08-483-554B-20	Sequence 20, Appl
16	176.2	3.2	6769	1	US-08-488-011B-20	Sequence 20, Appl
17	176.2	3.2	6769	3	US-08-850-727-20	Sequence 20, Appl
18	176.2	3.2	6769	5	PCT-US95-10202-20	Sequence 20, Appl
19	176.2	3.2	6769	5	PCT-US95-10203-20	Sequence 20, Appl
20	176.2	3.2	6769	5	PCT-US95-10220-20	Sequence 20, Appl
21	175.8	3.2	21784	4	US-09-491-356C-1	Sequence 3, Appli
22	175.8	3.2	55298	4	US-09-491-356C-1	Sequence 1, Appli
23	175.4	3.2	9365	4	US-09-608-285A-8	Sequence 8, Appli
24	175.4	3.2	9365	4	US-09-350-836B-8	Sequence 8, Appli
25	175.4	3.2	9365	4	US-09-370-265-8	Sequence 8, Appli
26	175.4	3.2	9365	4	US-09-557-800C-8	Sequence 8, Appli
27	175.4	3.2	9365	4	US-09-370-625A-8	Sequence 8, Appli
28	175.4	3.2	14747	4	US-09-608-285A-42	Sequence 42, Appl
29	175.4	3.2	14747	4	US-09-557-800C-42	Sequence 42, Appl
30	175.4	3.2	15977	4	US-09-608-285A-59	Sequence 59, Appl
31	175.4	3.2	53332	3	US-09-801-861-3	Sequence 3, Appli
32	175.4	3.2	72928	3	US-09-009-913-1	Sequence 1, Appli
33	175	3.2	35060	3	US-08-814-095-7	Sequence 7, Appli
34	174.8	3.2	14581	4	US-08-520-373D-4	Sequence 4, Appli
35	174.8	3.2	22481	5	US-08-367-841A-43	Sequence 43, Appl
36	174.8	3.2	22481	5	PCT-US95-07201-43	Sequence 43, Appl
37	174.8	3.2	22484	4	US-09-875-223-2	Sequence 2, Appli
38	174.8	3.2	22484	4	US-09-875-114-2	Sequence 2, Appli
39	174.8	3.2	84495	4	US-09-797-906-3	Sequence 3, Appli
40	174.4	3.2	51719	4	US-09-918-686-2	Sequence 2, Appli
41	174.4	3.2	92139	4	US-09-918-686-1	Sequence 1, Appli
42	174.2	3.2	45546	4	US-09-146-053-6	Sequence 6, Appli
43	174	3.1	99500	4	US-09-798-096-10	Sequence 10, Appl
44	173.8	3.1	4086	4	US-09-702-705-1801	Sequence 1801, Ap
45	173.8	3.1	4086	4	US-09-736-457-1801	Sequence 1801, Ap

ALIGNMENTS

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RESULT 1
US-09-016-434-785
; Sequence 785, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
;    APPLICANT: Janice Au-Young
;    APPLICANT: Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES: 1490
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;       STREET: 3174 PORTER DRIVE
;       CITY: PALO ALTO
;       STATE: CALIFORNIA
;       COUNTRY: USA
;       ZIP: 94304
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/016,434
;       FILING DATE: HEREWITH
;       CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;       CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Zeller, Karen J.
;       REGISTRATION NUMBER: 37,071
;       REFERENCE/DOCKET NUMBER: PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (650) 855-0555
;       TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 785:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH: 244 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;    IMMEDIATE SOURCE:
;       LIBRARY: HNT2AGT01
;       CLONE: 488190
US-09-016-434-785

  Query Match             4.4%;  Score 244;  DB 4;  Length 244;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-52;
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Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Zy 2373 CAGAATCAGGATGAAGATTGCAATGAAAAGAAGATGGCTGCCATGAAAGTGAGCCATCAGTG 2432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CAGAATCAGGATGAAGATTGCAATGAAAAGAAGATGGCTGCCATGAAAGTGAGCCATCAGTG 60

Zy 2433 ACGACTGAGGCTGTGCACTACCTATACATCCAGATGAGTACTGTGAGAAGAGCACTTTA 2492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ACGACTGAGGCTGTGCACTACCTATACATCCAGATGAGTACTGTGAGAAGAGCACTTTA 120

Zy 2493 CGAGACACCATTGACCAGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTCGA 2552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CGAGACACCATTGACCAGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTCGA 180

Zy 2553 GAGATTCTGATGGATTAGCTTATATCCATGAGAAAGGAAATGATTCACCGGGATTGAAG 2612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GAGATTCTGATGGATTAGCTTATATCCATGAGAAAGGAAATGATTCACCGGGATTGAAG 240

Zy 2613 CCTG 2616
             |||
Db  241 CCTG 244
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RESULT 2
US-09-750-580-1/c
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89.US2.CIP
; CURRENT APPLICATION NUMBER: US/09/750,580
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR APPLICATION FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB00/0101
; PRIOR APPLICATION FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR APPLICATION FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR APPLICATION FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR APPLICATION FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR APPLICATION FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 81001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10946..12946
; OTHER INFORMATION: 5' regulatory region
; NAME/KEY: exon
; LOCATION: 12947..12958
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 13470..13526
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 13641..13752
; OTHER INFORMATION: exon 3
; NAME/KEY: exon

; LOCATION: 14271..15968
; OTHER INFORMATION: exon 4
; NAME/KEY: misc_feature
; LOCATION: 15969..17969
; OTHER INFORMATION: 3' regulatory region
; NAME/KEY: allele
; LOCATION: 1239
; OTHER INFORMATION: 20-828-311 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 12347
; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 15241
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 42218
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 45442
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 77058
; OTHER INFORMATION: 20-853-415 : polymorphic base C or T
; NAME/KEY: primer_bind
; LOCATION: 929..949
; OTHER INFORMATION: 20-828.pu
; NAME/KEY: primer_bind
; LOCATION: 1357..1377
; OTHER INFORMATION: 20-828.rp complement
; NAME/KEY: primer_bind
; LOCATION: 12029..12050
; OTHER INFORMATION: 17-42.pu
; NAME/KEY: primer_bind
; LOCATION: 12581..12603
; OTHER INFORMATION: 17-42.rp complement
; NAME/KEY: primer_bind
; LOCATION: 14992..15012
; OTHER INFORMATION: 17-41.pu
; NAME/KEY: primer_bind
; LOCATION: 15460..15482
; OTHER INFORMATION: 17-41.rp complement
; NAME/KEY: primer_bind
; LOCATION: 42070..42090
; OTHER INFORMATION: 20-841.pu
; NAME/KEY: primer_bind
; LOCATION: 42572..42591
; OTHER INFORMATION: 20-841.rp complement
; NAME/KEY: primer_bind
; LOCATION: 45328..45347
; OTHER INFORMATION: 20-842.pu
; NAME/KEY: primer_bind
; LOCATION: 45863..45883
; OTHER INFORMATION: 20-842.rp complement
; NAME/KEY: primer_bind
; LOCATION: 76644..76664
; OTHER INFORMATION: 20-853.pu
; NAME/KEY: primer_bind
; LOCATION: 77166..77185
; OTHER INFORMATION: 20-853.rp complement
; NAME/KEY: primer_bind
; LOCATION: 1220..1238
; OTHER INFORMATION: 20-828-311.mis
; NAME/KEY: primer_bind
; LOCATION: 1240..1258
; OTHER INFORMATION: 20-828-311.mis complement
; NAME/KEY: primer_bind
; LOCATION: 12328..12346
; OTHER INFORMATION: 17-42-319.mis
; NAME/KEY: primer_bind
; LOCATION: 12348..12366
; OTHER INFORMATION: 17-42-319.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15222..15240

OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
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LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match   3.4%;   Score 187.6; DB 4; Length 81001;
Best Local Similarity   71.1%;   Pred. No. 3.2e-36;
Matches 263; Conservative 0; Mismatches 104; Indels 3; Gaps 1;

Qy   5084 TCATCATAATTAAATTAAATTCTAAGAAGAGCTGGGTGCAGTGGCTCACACCTTTAA 5143
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Db   65068 TTACCCTGATTTTACAAATAAGGAAATTGTGTGGCCAGTGCAGTGGCTCACGCCTGTAA 65009

Qy   5144 TCCCAGCACTTTGGGAAGCCAAGGCAGGAGAACTGCTTGAAACCAGGAGTTTGAGACCAG 5203
           ||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   65008 TCCCAGCACTTTGGGAGGCCAAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCAG 64949

Qy   5204 CCTGAGCAACAAGCAAGCAAGACCCCATCTCTATAAAAATCAAAAAATTAGCCGGGCATGGT 5263
           ||||||| |||||||||||||||||||||||||||| |||||||| ||||
Db   64948 CCTGGCCAACATGGTGAAACCCCGTCTCTATTAAAAATACAAAAATTAGCCGGGCATGGT 64889

Qy   5264 GGCACATGCCTGTAGTCCCAGCTACTCCAGAGGCTGAG--ATGGATCATCTGAGCCTCA 5320
           |||||||||||||||||||||||||||| | ||||||| ||||||| ||||||
Db   64888 GGCAGGAGCCTGTAATCCCAGCTACTCCAGGAGGCTGAGGCAGGAGAATCACTTGAACCCG 64829

Qy   5321 GGAGGTTGAGGCTGCAGTGAGCTGTGACTGCGCCACTGCACTCCAGCTGGGACAACAGA 5380
           |||||||||||| |||||||||||||||||| ||||||||||||| |||||||
Db   64828 GGAGGCGGAGGTTGCAGTGAGCTGAGATTGCGCCACTGCACTCCAGCCTGGGACAAGA 64769

Qy   5381 GCAAGACCCTGTCTTAAAAAAAAAAGAAAAAATTTTTTTCTAAGAAGCTGTCCTA 5440
           |||||||| ||||||||||||||||||||||||||||| ||||||||
Db   64768 GCGAGACTCTGTATCAAAAAAAAAACAAAAAATAAATAAATAAGGAAACTGTGGCTCAG 64709

Qy   5441 CAAAGTTGAG 5450
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Db   64708 AGAAGTTAAG 64699

RESULT 3
US-09-817-180-3
; Sequence 3, Application US/09817180
; Patent No. 6345584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Human
US-09-817-180-3

Query Match   3.4%;   Score 185.6; DB 4; Length 15297;
Best Local Similarity   75.0%;   Pred. No. 3.8e-36;
Matches 246; Conservative 0; Mismatches 79; Indels 3; Gaps 1;

Qy   5092 ATTTAAAATTAAATTCTAAGAAGAGCTGGGTGCAGTGGCTCACACCTTAATCCCAGCA 5151
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11802 ATCTGTACAAAAATACAAAAATTAGACTGGGCACGGTGGCTCACACCTGTAATCCCAGCA 11861

Qy   5152 CTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCTGAGCA 5211
           |||||||||||||||||| ||| |||||||||||||||||| |||||||||||
Db   11862 CTTTGGGAGGCCGAGGCAGGTGGATCACCTGTGGTCAGGAGTTTGAGACCAGCAGACCA 11921

Qy   5212 ACAAAGCAAGACCCCATCTCTATAAAAACTAAAAAAATTAGTTGGGCATGGTGGCACATG 5271
           ||||||||||||||||||||||||||||| ||||||||||||| |||||||||||||
Db   11922 ACATGTGAAACCCCATCCCATCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGCACGTG 11981

Qy   5272 CCTGTAGTCCCAGCTACTCCAGAGGCTGAGATG---GATCATCTGAGCCTCAGGAGGTTG 5328
           ||||| |||| ||||||| ||||||||||||||| |||||||| ||||||||||
Db   11982 CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCTGGGAGAATTGCTTGAACCCAGGAGGCGG 12041

Qy   5329 AGGCTGCAGTGAGCTGTGACTGCGCCACTCTCGGACACAGAGCAAGACC 5388
           |||||||||||||||||||| ||||||||||||||||||
Db   12042 AGGCTGCAGTGAGCCGAGATTGTGCCACTGCACTCCAGCCTGGGCGACAAGAGTGAAACT 12101

Qy   5389 CTGTCTTAAAAAAAAAAAGAAAAAAAAAAA 5416
           ||||||| ||||||||||||| ||||
Db   12102 CCATCTCAAAAAAAAAACCAAAAAACAAA 12129

RESULT 4
US-10-003-295-3
; Sequence 3, Application US/10003295
; Patent No. 6686187
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-3

Query Match   3.4%;   Score 185.6; DB 4; Length 15297;
Best Local Similarity   75.0%;   Pred. No. 3.8e-36;

Matches 246; Conservative 0; Mismatches 79; Indels 3; Gaps 1;

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Qy   5092  ATTTAAAATTAAATTCTAAGAAGAGAGGCTGGGGTGCAGTGGCTCACACCTTTAATCCCAGCA  5151
           |||||   |||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  11802  ATCTGTACAAAAAAATACAAAAAATTAGACTGGGCACGGTGGCTCACACCTGTAATCCCAGCA  11861

Qy   5152  CTTTGGGAAGCCAAGGCAGGAGGAAGACTTGCTTGAAACCAGGAGTTGAGACCAGCCTGAGCA  5211
           ||||||| |||||| ||| |||  | |||||||||||||||||||||||||||||||||||||
Db  11862  CTTTGGGAGGCCGAGGCGGGTGGATCACCTGTGGTCAGGAGTTGAGACCAGCCAGCACCACCA  11921

Qy   5212  ACAAAGCAAGACACCCCATCCTATAAAAACTACTAAAAAATTAGTAGGGCATGGTGGCACATG  5271
           |||   ||| |||||||||||   ||  ||||  ||||||||||||   ||||||||||||||
Db  11922  ACATGGTGAAAACCCCATCTCCTACTACAAAAATACAAAAAATTAGCCAGGCATGGTGGCACGTG  11981

Qy   5272  CCTGTAGTCCAGCTACTCCAGAGGCTGAGATG---GATCATCTGACCTCAGGAGGTTG  5328
           |||||| ||||||||||   ||||||||||    |||||| |||  ||||||||| ||
Db  11982  CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCTGGGAGGATCAATTGCTTGAACCCAGGAGTGAAACT  12041

Qy   5329  AGGGTGCAGTGAGCTGTGACTGCGCCACTGCACTCCAGTCTCTGGGACAACAGAGCAAGACC  5388
           |||||||||||| |||||| ||| ||||||| ||| ||||||||||| |||||||  |||||
Db  12042  AGGGTGCAGTGAGCCGAGATTGTGCCACTGCACTCCCAGCCTGGGCGACAGAGTGAAACT  12101

Qy   5389  CTGTCTTAAAAAAAAGAAAAAAAA  5416
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Db  12102  CCATCTCAAAAAAAAACCAAAAAACAAAA  12129
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RESULT 5
US-09-128-155-17/c
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 3.4%; Score 185.6; DB 3; Length 176373;
Best Local Similarity 68.3%; Pred. No. 1.6e-35;
Matches 302; Conservative 0; Mismatches 134; Indels 6; Gaps 3;

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Qy   5081  CATTCATCATAATTTAAAATTAAAATTCTAAGAAGAGAGGCTGGGGTGCAGTGGCTCACACCTT  5140
           ||   ||||  ||  |||  ||||||||||||  |   || |||||||||||||||||||||||
Db 115379  CATACTAGTTTTGTTTCACTTAAATAGTTATTGAGGGCAGGGGCCAGATCGCTTAATGAGTTATTGAGGGGCAGG...  115320

Qy   5141  TAATCCCAGCACTTTGGGAAGCCAAGGCAGGAGGATCTGCTTGAAACCAGGAGTTTGAGAC  5200
           |||||||||||   |||||||| ||||| |||     |  ||||  ||| |||||||||||
Db 115319  TAATCCCAACACTTTGGGAAGCCGAGGCGGGGGGATCACGCTTGAGCCCAGGAGTTTGAGAC  115260

Qy   5201  CAGCCTGAGCAACAAAGCAAGACCCCATCTCTATAAAAAATAAAATACAAAAATTAGTTAGGGCAT  5260
           ||||| |||  ||| |||  ||| |||| |||  |||||  |||| |||||||| |||||||||||
Db 115259  CAGCCTG-GTAACATGTGAAACCCCATCCTCTACAAAAATACAAAAATTAGCCAGGCATGGTGGCAT  115201

Qy   5261  GGTGGCACATGCCTGTAGTCCTGAGTCCCAGCTACTCCAGAGGCTAGGCAGGAGAGAAAGCTTGAGC  5316
           ||||||||| || |||||||| || ||| ||||||||||   |||||| |||||||||||||||||
Db 115200  GGTGGCGTGTGTGCCTGTGCCTGTGGACCCCAGCTACTCCATGAGGCAGGAGGCAGGAAAGCTTGAGC  115141
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Query Match 3.3%; Score 181.2; DB 4; Length 44848;
Best Local Similarity 76.1%; Pred. No. 9.2e-35;
Matches 236; Conservative 0; Mismatches 73; Indels 1; Gaps 1;

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Qy   5317  CTCAGGAGGTTGAGGCTGCAGTGAGCTGTGACTGCGTGAGCTGGGCCACTGCACCTCCAGTCTCTGGGACAA  5376
           |||| ||||| |||| |||||||||||| |||  |||||||||||||||||||  |||||||||||||||||
Db 115140  CTCAAGAGGTGGAGGGCTGCAGTGAGCTGCAGATCAGCCACTGCAGTGAGTCCAGCCTGAG-CAA  115082

Qy   5377  CAGAGCAAGACCCTGTCTTAAAAAAAAGAGAAAAAAAATTTTTTTCTTAAGAGAGCTGT  5436
           ||||  |||||| ||||| |||||||| |  ||  |||  | ||| || ||||  |  |
Db 115081  CAGAACAAGATCCTGTCTCAAAAAAAATAAATAAAGTAAATAAAACTATTT  115022

Qy   5437  CCTACAAGTTGAGCTTTGTTAGTTTTTCATGTGAATATTTATATATTATCTTTTTGG  5496
           |||||||||| |  ||  |||| || |||||||||||   |||||  |  ||| |||
Db 115021  GATTACAAGTTTATAATTGTGTCTTTCTGGTGAATTAAACCTTTCATCATCACAAGTTGA  114962

Qy   5497  GATATAATAAATGCTTTCATAT  5518
           |||  ||||| ||| ||||
Db 114961  CTCACAATAATGCATCTTATCT  114940
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Qy   5115  AGGGTGGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTGGGAAGCCAAGGCAGGCAGGAAG  5174
           ||| ||||||||||||||||  || |||||||||||||||||||||| ||||| ||||||| ||
Db  22625  AAGCTGGGTGCAGTGGCTCATGCGTGTAATCCCAGCACTTTGGGAGGCTGAGGCAGGCAGTGG  22566

Qy   5175  ACTGCTTGAAACCAGGAGTTGAGACCAGCAACAGAGCAAGACCCCATCTCTAT  5234
           |   |  | |  ||||||||| ||||||  |||  || ||||  |||||| ||
Db  22565  ATCACCTGAGGTCAAGAGTTCAAGACCAGCCTGCCCAATATGGTGAAACCCCGTCTCTAC  22506

Qy   5235  AAAAACTAAAAAAAATTAGTTGGGCACATGCGTGGCAGTGGCTGTAGTCCCAGCTACTCCAGA  5294
           |||||  | ||||||||||  |||  | || ||||| ||||||||||||| ||||||||| ||
Db  22505  TAAAAATACAAAAAATTAGCCGGGTGGGGTGCAGTGGCTGTAGTCCCAGCTACTCCTGGGA  22446

Qy   5295  GGCTGAGATGGATCATCATCTGAGCCTGAGCTGAGGTTGAGGCTGCAGTGAGCTGTGACTGCGCC  5354
           ||||||||  ||  | | ||||| |||  ||| ||||| | |||||||||||| ||| |||||||
Db  22445  GGCTGAGAGCAGAATTGCTCAAACCCGGAGGTGGAGGTTGCAGTGAGCCGGAGATTGTGCC  22386

Qy   5355  ACTGCACTCCAGTCTCTGGGACAACAGAGCAACAGAGCAAGACCCTGTCTTAAAAAAGAAAAAAA  5414
           |||||||| | |  |||||| ||||| ||||| ||||||||||  ||||| |||||||||  |||
Db  22385  ACTGCACTGCGAGCCTGGG-TAACAGCAGCAAGACTTCTGTCTCAAAAAAAAAAAAATTAAC  22327

Qy   5415  AATTTTTTTT  5424
           ||| |  |||
Db  22326  TATTTAATAT  22317
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APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001178
CURRENT APPLICATION NUMBER: US/09/813,817
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3

Query Match   3.2%;   Score 179; DB 4;   Length 59065;
Best Local Similarity   74.3%;   Pred. No. 3.9e-34;
Matches 240;   Conservative   0;   Mismatches   80;   Indels   3;   Gaps   1;

Qy   5097 AAATTAAATTCTAAGAAGACGTGGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTG 5156
                ||| |||||||||| |||||||| ||||||| ||||||||||||||||||||||||||
Db   32283 ACATTTAATCCTCACTGCAGGCCAGGCGATAGTGGCTCACACCTGTAATCGCAGCACTTCG 32342

Qy   5157 GGAAGCCAAGGCGAGGCGGATCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCAACAAA 5216
                ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   32343 GGAGGCCAAGGCGGGCGGATCACTCTTGAGGTCGGGAGTTCGAGACCAGCCTCACCAACATG 32402

Qy   5217 GCAAGACCCCATCTCTATAAAAAACTAAAAAATTAGTTGGGCATGGTGGCACATGCCTGT 5276
                ||| |||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db   32403 GGGAAACCCCGTCTCTACTAAAAATAGAAAAATTAGCCGGGTGTGGTGGCATGCGCCAGT 32462

Qy   5277 AGTCCCAGTACTCCAGAGGCTGAGATGG---ATCATCTGAGCCTCAGGAGGTTGAGGCT 5333
                |||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   32463 AATCCCAGCTACTCAGGAGGCTGAGGTGGGAAAATCACTTGAACTCGGGAGGCAGAGGTT 32522

Qy   5334 GCAGTGAGCTGTGACTGCGCGCCACTGCACTCTCGGCACACCTGTC 5393
                ||||||||||||||||||||||||||||||||||||||||||||||
Db   32523 GCAGTGAGCCGAGATTGTGCCACTGCACTCCAGCCTGGGCGATAAGAGCAAAATTCCATC 32582

Qy   5394 TTAAAAAAAAGAAAAAAAGA 5416
                ||||||||||||||||||||
Db   32583 TCAAAAAAAAAAGAAAAAGAA 32605

RESULT 8
US-09-978-197-3
; Sequence 3, Application US/09978197
; Patent No. 6403353
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001178DIV
; CURRENT APPLICATION NUMBER: US/09/978,197
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/813,817
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-978-197-3

Query Match   3.2%;   Score 179; DB 4;   Length 59065;
Best Local Similarity   74.3%;   Pred. No. 3.9e-34;
Matches 240;   Conservative   0;   Mismatches   80;   Indels   3;   Gaps   1;

Qy   5097 AAATTAAATTCTAAGAAGACGTGGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTG 5156
Db   32283 ACATTTAATCCTCACTGCAGGCCAGGCGATAGTGGCTCACACCTGTAATCGCAGCACTTCG 32342

Qy   5157 GGAAGCCAAGGCGAGGCGGATCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCAACAAA 5216
                ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   32343 GGAGGCCAAGGCGGGCGGATCACTCTTGAGGTCGGGAGTTCGAGACCAGCCTCACCAACATG 32402

Qy   5217 GCAAGACCCCATCTCTATAAAAAACTAAAAAATTAGTTGGGCATGGTGGCACATGCCTGT 5276
                ||| |||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db   32403 GGGAAACCCCGTCTCTACTAAAAATAGAAAAATTAGCCGGGTGTGGTGGCATGCGCCAGT 32462

Qy   5277 AGTCCCAGTACTCCAGAGGCTGAGATGG---ATCATCTGAGCCTCAGGAGGTTGAGGCT 5333
                |||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   32463 AATCCCAGCTACTCAGGAGGCTGAGGTGGGAAAATCACTTGAACTCGGGAGGCAGAGGTT 32522

Qy   5334 GCAGTGAGCTGTGACTGCGCGCCACTGCACTCTCGGCACACCTGTC 5393
                ||||||||||||||||||||||||||||||||||||||||||||||
Db   32523 GCAGTGAGCCGAGATTGTGCCACTGCACTCCAGCCTGGGCGATAAGAGCAAAATTCCATC 32582

Qy   5394 TTAAAAAAAAGAAAAAAAGA 5416
                ||||||||||||||||||||
Db   32583 TCAAAAAAAAAAGAAAAAGAA 32605

RESULT 9
US-09-341-587-8/c
; Sequence 8, Application US/09341587
; Patent No. 6346606
; GENERAL INFORMATION:
; APPLICANT: Mollenhauer, Jan
; TITLE OF INVENTION: Protein Containing an SRCR Domain
; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341,587
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096
; EARLIER FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3166
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-8

Query Match   3.2%;   Score 177.6; DB 4;   Length 3166;
Best Local Similarity   76.9%;   Pred. No. 1.6e-34;
Matches 243;   Conservative   0;   Mismatches   69;   Indels   4;   Gaps   2;

Qy   5102 AAATTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTGGGAGG 5161
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   888 AAGGTCAGAAAAGAGGCCCGGGTCAGTGGCTCACACCTGTAATCCCGGCACTTTGGGAGG 829

Qy   5162 CCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCAACAAAGCAAG 5221
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   828 CCTAGGCAGGCAGATCACTTGAAGTCAGGAGTTTGAGACCAGCCTGGCCAACATGATGAA 769

Qy   5222 ACCCATCTCTATAAAAACTAAAAAATTAGTTGGGCATGGTGGCACATGCCTGTAGTCC 5281
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   768 ACCCCGTCTCTACTAAAAATACAAAACTTAGCTGGGCATGGTCTTAGCCTGTCTAATCT 709

Qy   5282 CAGCTACTCCAGAGGCTGAGATGGATCA---TCTGAGCCTCAGGAGGCTGAGGTGCAGT 5338
                |||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   708 TAGCTACTAGGGAGGCTGAGGCAGGAGATCGCTTGAACCCGGGAGGCGGAGGTTGCAGT 649

Qy   5339 GAGCTGTGACTGCGCGCCACTGCACTCTCGGCACACCTGTCTAAA 5398
                ||||||||||||||||||||||||||||||||||||||||||||
Db   648 GAGTTGAGATTGTGCCACTGCACTCCAGCCTGGG-CAACAAAGCAAGCAAGACACTGTCTCAAA 590

Qy   5399 AAAAAAGAAAAAAA 5414
                ||||||||||||
Db   589 AAAAAAAAAAAAAA 574

RESULT 10
US-09-016-434-1449/c

; Sequence 1449, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;   STREET: 3174 PORTER DRIVE
;   CITY: PALO ALTO
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/016,434
;   FILING DATE: HEREWITH
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Zeller, Karen J.
;   REGISTRATION NUMBER: 37,071
;   REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 855-0555
;   TELEFAX: (650) 845-4166
; US-09-016-434-1449
; INFORMATION FOR SEQ ID NO: 1449:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4079 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GENBANK
;   CLONE: g727358
; US-09-016-434-1449

Query Match   3.2%;   Score 177.2;   DB 4;   Length 4079;
Best Local Similarity   74.5%;   Pred. No. 2.3e-34;
Matches 237; Conservative   0; Mismatches   78; Indels   3; Gaps   1;

Qy   5102 AAATTCTAAGAGAGAGGCTGGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTGGGAAG 5161
          ||||||| ||||| ||||||| |||||||||||||||||||||||||||||||||||||
Db   1786 AAAACATGAGTATTGGCCGGGTGTGGTGGTTCACACCTGTAATCTCAGTACTTTGGGAGG 1727

Qy   5162 CCAAGGCAGGAGAGACTGCTTGAAACCAGGAGTTTGAGACCAGCCTGAGCAACAAAGCAAG 5221
          ||||||||||| | |||||| ||||||||||||| ||||||||||| ||||||| ||
Db   1726 CCAAGGCAGGAGATGGATCAGATGAACCCAGGAGGTTCAAGACCAGCCAGCCTGGGCAACATGGTGAA 1667

Qy   5222 ACCCCATCTCTATAAAAACTAAAAAAATTAGTTGGGCATGGTGGCACGTGCCTGTAGTCC 5281
          ||||| |||| |||| ||||||||| ||||||| |||||| |||| ||| ||||||||
Db   1666 ATCCTGTCTTTACAAAAATACAAAAAATTAGCTGGGCATGTGGTGCATACCTGTGGTCC 1607

Qy   5282 CAGCTACTCCGAGGCGCGAGATG---GATCATCTGAGCCTCAGGAGGTTGAGGCTGCAGT 5338
          |||||| ||| |||| |||||| |||||||||| ||||||||||||||| |||||
Db   1606 CAGCAACTCGAGAGGCTGAGGTGGGAGAATCGTTAAGCCTGGAAGGTCGAGGCTGCAGC 1547

Qy   5339 GAGCTGTGACTGCGCCACTGCACTCCAGTCTGGGACAACAGAGCAAGACCCCTGTCTTAAA 5398
          |||||| |||||| ||||||| || ||||| ||||||||||||||||| |||||| |
Db   1546 GAGCTATGATTGCCACTGCACTTCAGTCTGGGCCGACCGGCCGACCCCTGTCTCTCAAC 1487

Qy   5399 AAAAAAAGAAAAAAAAA 5416
          ||||| |||||||||||
Db   1486 AACAACAACAACAACAA 1469

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LOCATION: 77058
OTHER INFORMATION: 20-853-415  : polymorphic base C or T
NAME/KEY: primer_bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
NAME/KEY: primer_bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer_bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.rp complement
NAME/KEY: primer_bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer_bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc_binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match              3.2%;   Score 176.8;  DB 4;   Length 81001;
Best Local Similarity   77.2%;   Pred. No. 1.7e-33;
Matches  241;  Conservative  0;  Mismatches  67;  Indels  4;  Gaps  2;

Qy  5098 AATTAAATTCTAAGAGAGAGCTGGGTGCAGTGGCTCACACCTTAATCCCAGCACTTGG 5157
         |||||| |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db 69814 AATTAAAGAGAAGAAAGTGGGGCTGGGCAGTGGCTCATGCATGTCATGTGCTTTGG 69873

Qy  5158 GAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCCTGAGCAACAAAG 5217
         |||||||||||| ||| ||||||||||||||||||||||||||||||||| ||  |||||
Db 69874 GAGGCTGAGGTGGGTAGGTTGCTTGAGCCCAGGAGTTTGAGACCAGCCTGGGCAACATAG 69933

Qy  5218 CAAGACCCCATCTCTATAAAACTAAAAAAATTAGTTGGGCATGGTGGCACATGCCTGTA 5277
         |||     ||||||||||||  ||| |||||||||||||||||||||||||||||||||
Db 69934 TGAGACCCTTGTCTCTTACAATAAGTTAAAAAAATTAGCTGGGCATGGTGGCACCCACCTGTA 69993

Qy  5278 GTCCCAGCTACTCCAGAGGCTGAGATGGA---TCATCTGAGCCTCAGGAGGTTGAGGCTG 5334
         |||||||||| |||||||||||||   |   ||||||||||||||||||||||||||||
Db 69994 GCCCCAGCTACTTGAGAGGGTGAGGTGGAAGGATCACTTGAGTCTGGGAGGTTGAGGCTG 70053

Qy  5335 CAGTGAGCTGTGACTGGCGCGCCACTCCAGTCTGGGAGCAACAGAGCAAGAGACCCTCTCT 5394
         ||||||||||||| ||| ||| ||||||||||||||| ||||  |||||||||||||||
Db 70054 CAGTGAGCTGTGATTGAGCCAGTCCACTCCAGCCAGGG-TGACAGAGTAAGACTCTGTCT 70112

Qy  5395 TAAAAAAAAAA 5406
         |||||||||||
Db 70113 CAAAAAAAAAA 70124
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COUNTRY: USA
ZIP: 20005
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,784
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-480-784-20

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Query Match     3.2%;   Score 176.2;  DB 1;  Length 6769;
Best Local Similarity   75.9%;   Pred. No. 5.5e-34;
Matches  245;   Conservative   0;   Mismatches  73;   Indels  5;   Gaps  2;

Qy   5098 AATTAAATTCTAAGAAGAGAGCTGGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTGG 5157
          ||||||      || |  | ||||| ||| ||||||||||  | ||||  | ||||||||||
Db   6559 AATTAAAAGTAAAGGGCAGGCCAGGCACAGTGGCTCAAGCTGTAACTGCAGCACTTTGG 6500
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RESULT 13
US-08-483-553-20/c
; Sequence 20, Application US/08483553
; Patent No. 5709999
; GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,553
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-483-553-20

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Best Local Similarity   75.9%;   Pred. No. 5.5e-34;

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REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-487-002-20

Query Match   3.2%;   Score 176.2; DB 1;   Length 6769;
Best Local Similarity 75.9%;   Pred. No. 5.5e-34;
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RESULT 15
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; Sequence 20, Application US/08483554B
; Patent No. 5747282
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavigian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
;   STREET: 1201 New York Avenue, N.W., Suite-1000
;   CITY: Washington
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 20005
; COMPUTER READABLE FORM:

Matches 245;   Conservative 0;   Mismatches 73;   Indels 5;   Gaps 2;

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RESULT 14
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; Sequence 20, Application US/08487002
; Patent No. 5710001
; GENERAL INFORMATION:
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Simard, Jacques
; APPLICANT: Emi, Mitsuru
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Durocher, Francine
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
;   STREET: 1201 New York Avenue, N.W., Suite 1000
;   CITY: Washington
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 20005
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/487,002
;   FILING DATE:
;   CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/409,305
;   FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/348,824
;   FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/308,104
;   FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/300,266
;   FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/289,221
;   FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ihnen, Jeffrey L.

Job time : 241 secs

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               OPERATING SYSTEM: PC-DOS/MS-DOS
               SOFTWARE: PatentIn Release #1.0, Version #1.30
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               FILING DATE: 07-JUN-1995
               CLASSIFICATION: 514
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               FILING DATE: 24-MAR-1995
          PRIOR APPLICATION DATA:
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               FILING DATE: 29-NOV-1994
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               FILING DATE: 02-SEP-1994
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               APPLICATION NUMBER: US 08/289,221
               FILING DATE: 12-AUG-1994
          ATTORNEY/AGENT INFORMATION:
               NAME: Ihnen, Jeffrey L.
               REGISTRATION NUMBER: 28,957
               REFERENCE/DOCKET NUMBER: 24884-109347
          TELECOMMUNICATION INFORMATION:
               TELEPHONE: 202-962-4810
               TELEFAX: 202-962-8300
     INFORMATION FOR SEQ ID NO: 20:
          SEQUENCE CHARACTERISTICS:
               LENGTH: 6769 base pairs
               TYPE: nucleic acid
               STRANDEDNESS: double
               TOPOLOGY: linear
          MOLECULE TYPE: DNA (genomic)
          HYPOTHETICAL: NO
          ANTI-SENSE: NO
          ORIGINAL SOURCE:
               ORGANISM: Homo sapiens
US-08-483-554B-20

Query Match      3.2%;   Score 176.2;  DB 1;  Length 6769;
Best Local Similarity  75.9%;   Pred. No. 5.5e-34;
Matches  245;  Conservative   0;  Mismatches  73;  Indels   5;  Gaps   2;

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Qy   5394 TTAAAAAAAAAGAAAAAAAAA 5416
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Db   6260 TCAAAAAAAAACAAACAAACAAA 6238
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Search completed: March 21, 2004, 22:18:51

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                    GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     March 21, 2004, 22:09:09 ; Search time 1231 Seconds
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Searched:       2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters:     4876514

Minimum DB seq length:  0
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Post-processing:  Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	5217.8	94.4	5305	15	US-10-258-106-33	Sequence 33, Appl
3	5040.8	91.2	5044	12	US-10-112-944-117	Sequence 117, App
4	5005.2	90.6	5094	12	US-10-174-333-138	Sequence 138, App
5	4733	85.7	4989	10	US-09-842-758-3	Sequence 3, Appli
6	4733	85.7	4989	12	US-10-174-333-3	Sequence 3, Appli
7	4462.4	80.8	4861	12	US-10-112-944-90	Sequence 90, Appl
8	4436.4	80.3	4438	12	US-10-425-114-26218	Sequence 26218, A
9	2928.8	53.0	2946	9	US-09-836-392-6	Sequence 6, Appli
10	2144.6	38.8	2200	9	US-09-925-301-184	Sequence 184, App
11	1716.4	31.1	1845	14	US-10-006-285-498	Sequence 498, App
12	886.8	16.1	897	14	US-10-204-887-29	Sequence 29, Appl
13	517.4	9.4	519	9	US-09-998-598-753	Sequence 753, App
14	373.4	6.8	471	14	US-10-006-285-340	Sequence 340, App
15	368.4	6.7	691	15	US-10-062-674-1525	Sequence 1525, Ap

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 18  353.4  6.4  416  12  US-10-112-944-596       Sequence 596, App
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 20   348   6.3  388  15  US-10-242-535A-22903    Sequence 22903, A
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 37  189.2  3.4  1212 10  US-09-948-783-92        Sequence 92, Appl
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ALIGNMENTS

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; Patent No. US20020132321A1
; GENERAL INFORMATION:
;  APPLICANT: COOK, WILLIAM J.
;  APPLICANT: KAPELLER-LIBERMANN, ROSANA
;  TITLE OF INVENTION: 14790, NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR
;  FILE REFERENCE: 38155-20002.00
;  CURRENT APPLICATION NUMBER: US/09/515,806
;  CURRENT FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
;  LENGTH: 5525
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (63)..(4991)
US-09-515-806-1

Query Match             100.0%;  Score 5525;  DB 9;  Length 5525;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  5525;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db   721 ACAGAACGGGCTGCCATTCTACACTGGAGGCTCTCGACTTTGTAGGGAAATGGTAAACATC 780

Qy   781 GGGCAAACTCCTCAGGAAGGTCTAGGCGAGAACGTCAGTATTCTCAGTATGTAATAGTGAAG 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGGCAAACTCCTCAGGAAGGTCTAGGCGAGAACGTCAGTATTCTCAGTATGTAATAGTGAAG 840

Qy   841 ATTCTCCTGGCTCTTGTGAAATTCGTGTATTTCAATATGGGAGTCCTGATCAGCTCATGG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATTCTCCTGGCTCTTGTGAAATTCGTGTATTTCAATATGGGAGTCCTGATCAGCTCATGG 900

Qy   901 TGCACAAGGGAAATGTATTGGCAGTGATGAACAACTTGGAAAATTAGTCTACAATGCTT 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TGCACAAGGGAAATGTATTGGCAGTGATGAACAACTTGGAAAATTAGTCTACAATGCTT 960

Qy   961 TGGAAACAGCCACTGGTGGCTTTGTTCTTGTTGTGATGGGGTCCTTCAGTGGTGCAGAAAA 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGGAAACAGCCACTGGTGGCTTTGTTCTTGTTGTGATGGGGTCCTTCAGTGGTGCAGAAAA 1020

Qy  1021 AAATGGGTCCATTCCTTACCAGTCAAGAAAAGAGAAGATTGATAAGTGCAAAAAAGCAGA 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 AAATGGGTCCATTCCTTACCAGTCAAGAAAAGAGAAGATTGATAAGTGCAAAAAAGCAGA 1080

Qy  1081 TTCAAGGAACAGAACAGAATTCAACTCACTCACTGGTAAAATTGAGCCATCCAAATGTAGTAC 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TTCAAGGAACAGAACAGAATTCAACTCACTCACTGGTAAAATTGAGCCATCCAAATGTAGTAC 1140

Qy  1141 GCTACCTTGCAATGGGGGTCTTCTTCCTGTCGCACACCTGAGCCACTCGGCTGGTGACAATGTCCCTGTGC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GCTACCTTGCAATGGGGGTCTTCTTCCTGTCGCACACCTGAGCCACTCGGCTGGTGACAATGTCCCTGTGC 1200

Qy  1201 AGCACATTAGTGGGGGTCTCCTGCTGCAACCACTCGAGCCCCATCCCTGTGC 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AGCACATTAGTGGGGGTCTCCTGCTGCAACCACTCGAGCCCCATCCCTGTGC 1260

Qy  1261 ATCAGCTTCGCAGGTACACAGCTCACACTCCGTCGTGTCAGGCCTTGATTATCTGCACAGCAATT 1320
```

Right column:

```
Db  1261 ATCAGCTTCGCAGGTACACAGCTCACAGTCCGTCGTGTCAGGCCTTGATTATCTGCACAGCAATT 1320

Qy  1321 CTGTGGTCATAAGGTCCTGAGTGCATCTAATGTCTTGGTGATGCGAAGCACCGTCA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 CTGTGGTCATAAGGTCCTGAGTGCATCTAATGTCTTGGTGATGCAGAAGCACCGTCA 1380

Qy  1381 AGATTACGGACTATAGCATTTCTAAGGCCTGCAGACATTTGCAAGGAGGATGTGTTTG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 AGATTACGGACTATAGCATTTCTAAGGCCTGCAGACATTTGCAAGGAGGATGTGTTTG 1440

Qy  1441 AGCAAACCCGAGTTCGTTTAGTGACAATGACAATGTCCTGCCTTATAAACGGGAAGAAGGAG 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 AGCAAACCCGAGTTCGTTTAGTGACAATGTCTGCCTTATAAAACGGGAAGAAGGAG 1500

Qy  1501 ATGTTTGGCGTCTTCTGCCTTCGCTGTCCCTCAGCCAGGACACAGGAATGTGGAGAGT 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 ATGTTTGGCGTCTTCTGCCTTCGCTGTCCCTCAGCCAGGACACAGGAATGTGGAGAGT 1560

Qy  1561 ACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGATTTTCTAAAGAAATGTG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 ACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGATTTTCTAAAGAAATGTG 1620

Qy  1621 TGTCTTGATGACAAGGAAAAGATGGAGTCCCAGCAGTTGTTGAAACACAGCTTTATAA 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TGTGCTTGGATGACAAGGAAAAGATGGAGTCCCAGCAGTTGTTGAAACACAGCTTTATAA 1680

Qy  1681 ATCCCCAGCCAAAAAATGCCTCTAGTGCAACCGGCTACCCCAGTGCTGCCTTCTTTGAGACGACAC 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 ATCCCCAGCCAAAAAATGCCTCTAGTGCAACCGGCTACCCCAGTGCTGCCTTCTTTAGTGAGACGAC 1740

Qy  1741 ATGTTGAGACTGTTATTCCCGATACTTCTCATTGAGTTTGAAGAATTACAACTTCTTGGTAAAGGAG 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 ATGTTGAGACTGTTATTCCCGATACTTCTCATTGAGTTTGAAGAATTACAACTTCTTGGTAAAGGAG 1800

Qy  1801 AGAGACAGTTTTCCCGACAACATTGTGCGCTACTACAACGGCCTGATCTGAGCGGCACG 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 AGAGACAGTTTTCCCGACAACATTGTGCGCTACTACAACGGCCTGATCTGAGCGGCACG 1860

Qy  1861 CTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTCGTGCTGCTACGCAGTGAAGC 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 CTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTCGTGCTGCTACGCAGTGAAGC 1920

Qy  1921 GCATCCCATCAACCGGCCAGCCGGCCGGCCGGGATCAAGGGGCGAAGTGACACTGC 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 GCATCCCATCAACCGGCCAGCCGGCCGGCCGGGATCAAGGGGCGAAGTGACACTGC 1980

Qy  1981 TGTCACGGCTGCACCATGGCACCCATCTCCGGCTCGAGTGGAGCACTTCGGGGCGCCA 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 TGTCACGGCTGCACCATGGCACCCATCTCCGGCTCGAGTGGAGCACTTCGGGGCGCACG 2040

Qy  2041 AGCGGCCGCGGGGACCGGGGACCGGCGGCAGCCGCGGCGACACAGACCC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 AGCGGCCGCGGGGACGGGGACCGGCGGCAGCCGCGGCGACACAGACGACC 2100

Qy  2101 GAGCTGCACCGCGGGCAGCAGCCGGACGACGCGGCCGGCCG 2160
         |||||||||||||||||||||||||||||||||||||||||
Db  2101 GAGCTGCACCGCGGGCAGCAGCCGGACGACGCGGCCGCCCG 2160

Qy  2161 CGCCGCCACCATCTCCGGCCATGGAGCTCGGTGAGTCGAGCGGCGCACG 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 CGCCGCCACCATCTCCGGCCATGGAGCTCGGTGAGTCGAGCGGCGCACG 2220

Qy  2221 GTGCCCGTTTCCCGCGTCCTTCCTCCCCAGCTCTTCCTGCTTCAGATTCTGAAAGTGATATTA 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GTGCCCGTTTCCCGCGCCTTCCTCCCCAGCTCTTCCTGCTTCAGATTCTGAAAGTGATATTA 2280

Qy  2281 AGCACAGGTGGCGTCTTCTCTCCTGCTTCTTCCTGCAGTTCCTGCTTCAGATTCTGAAAGTGATTATTA 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 AGCACAGGTGGCGTCTTCTCTCCTGCCACACCTGAGCCACTCGGCTGGTGACAATGTCCCTGTGC 2340

Qy  2341 TCTTTGACAATGAAGGATGAAGAACAGTAAAAGTCAGAATCAGAATCAGGAAGAATTGCAATGAAA 2400
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This page is a nucleotide sequence alignment between two sequences labelled "Qy" and "Db", presented in a rotated (landscape) two-column layout. Each block shows a query row (Qy), a match line (| | |), and a database row (Db), with flanking position numbers.

Left column (positions 2341–3480):

```
Db  2341 TCTTTGACAATGAAGAATGAGAACAGTAAAAGTCAGAATCAGGATGAGCGACTGTGCACTACCTATACA 2400
Qy  2401 AGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGCTGTGCACTACCTATACA 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 AGAATGGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGCTGTGCACTACCTATACA 2460
Qy  2461 TCCAGATGGAGTACTGTGCAGAAGAGCACTTACGAGAACACCATTGACCAGGGACTGTATC 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 TCCAGATGGAGTACTGTGAGAAGAGCACTTACGAGGACACCATTGACCAGGGACTGTATC 2520
Qy  2521 GAGACACCGTCAGACTCTGGAGGCTTTTCGAGAGATTCTGGATGATGAATTAGCTTATATCC 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 GAGACACCGTCAGACTCTGGAGGCTTTTCGAGAGATTCTGGATGATGAATTAGCTTATATCC 2580
Qy  2581 ATGAGAAAGGAATGATGATTCACCCGGGATTTGAAGCCTGTCAACATTTTTTGGATTCGATG 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 ATGAGAAAGGAATGATGATTCACCCGGGATTTGAAGCCTGTCAACATTTTTTGGATTCGATG 2640
Qy  2641 ACCATGTGAAAAATAGGTGATTTTCGTTTCGGACAAGACCATCTAGCCTTTTCTGCTGACA 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 ACCATGTGAAAAATAGGTGATTTTCGTTTCGGACAAGACCATCTAGCCTTTTCTGCTGACA 2700
Qy  2701 GCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCCTTCAGTCACTTAACTG 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 GCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCCTTCAGTCACTTAACTG 2760
Qy  2761 GGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGGAAGCACCAAATCTGCAT 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 GGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGGAAGCACCAAATCTGCAT 2820
Qy  2821 ACAACCAGAAAGTGGATCTTCAGCCTCGGAATTATCTCTTGATGTCCTATCACC 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 ACAACCAGAAAGTGGATCTTCAGCCTCGGAATTATCTCTTGATGTCCTATCACC 2880
Qy  2881 CCATGTCAGGGCTTCAGAAAGGATCTTTGTTCCAACCAACTCAGAGAATCCCACTTCGC 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 CCATGTCACGGCTTCAGAAAGGATCTTTGTTCCAACCAACTCAGAGAATCCCACTTCGC 2940
Qy  2941 CTAAGTTTCCAGAAGACTTTGACGATGAGAGCAAAAATCAGTCATCTCCT 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 CTAAGTTTCCAGAAGACTTTGACGATGAGAGCAAAAATCAGTCATCTCCT 3000
Qy  3001 GGGCTGTTGAACCACGATCCAGCAAAACGGCCCACGAACTGCTCAAGAGTGAGC 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 GGGCTGTTGAACCACGATCCAGCAAAACGGCCCACGAACTGCTCAAGAGTGAGC 3060
Qy  3061 TGCTGCCCCCACCCCCAGATGGAGAGTCAGAGTCCATGAAGTGCATGAAGACGCTGA 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 TGCTGCCCCCACCCCCAGATGGAGAGTCAGAGTCGCTGCATGAAGTGCTGCACGCGCTGA 3120
Qy  3121 CCAACGTGGATGGAGAGGCTACCCGCACCATGAGGCCCAGATCTTCTCGCCAGCGCATCT 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 CCAACGTGGATGGAGAGGCTACCCGCACCATGAGGCCCAGATCTTCTCGCCAGCGCATCT 3180
Qy  3181 CCCCTGCCATCGATTACACCTTACACCCTGCTTCCACTACTGCTTCCAATCCGTA 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CCCCTGCCATCGATTACACCTTACACCCTGCTTCCACTACTGCTTCCAATCCGTA 3240
Qy  3241 CAGCCAAGATGCAGCAGCATGTGTGAAACCATCATCCGCATCTTAAAAAGACATGAG 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CAGCCAAGATGCAGCAGCATGTGTGAAACCATCATCCGCATCTTAAAAAGACATGAG 3300
Qy  3301 CTGTTCAGTTGTACTCCACTACCCGCTTCCCGAAACAGACAAATATGAGCACAACG 3360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 CTGTTCAGTTGTACTCCACTACCCGCTTCCCGAAACAGACAAATATGAGCACAACG 3360
Qy  3361 AAGCTGCCCATTCATGGACCACAGCGGATGCTGGTGGTGATGCTTCCTTTTGACCTGCGGA 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 AAGCTGCCCATTCATGGACCACAGCGGATGCTGGTGGTGATGCTTCCTTTTGACCTGCGGA 3420
Qy  3421 TCCCTTTTGCAAGATATGTGGCAAGAAGAATAATATTGAATTTAAAAACGATACTGCATAG 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 TCCCTTTTGCAAGATATGTGGCAAGAAGAATAATATTGAATTTAAAAACGATACTGCATAG 3480
```

Right column (positions 3481–4560):

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Qy  3481 AACGTGTGTTCAGGCCGCCGCCAAGTTAGATCGATTCATCCCAAAGAACTTCATCCCAAAGAACTTCTGAAATTATCTACA 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 AACGTGTGTTCAGGCCGCCGCCAAGTTAGATCGATTCATCCCAAAGAACTTCATCCCAAAGAACTTCTGAAATTATCTACA 3540
Qy  3541 CATTTGATATTGTCACTTCTACCACCAACAGCTTCTGCCCACTGCTGAAATTATCTACA 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CATTTGATATTGTCACTTCTACCACCAACAGCTTCTGCCCACTGCTGAAATTATCTACA 3600
Qy  3601 CTATCTATGAAATCATCCAAGAGTTTCAGCACTTCAGGAAGAAATTACAGTATTTATT 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CTATCTATGAAATCATCCAAGAGTTTCAGCACTTCAGGAAGAAATTACAGTATTTATT 3660
Qy  3661 TGAACCATACCATGTTATTGAAAGCAATACTCTTACACTGTGGGATCCCAGAAGATAAAC 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 TGAACCATACCATGTTATTGAAAGCAATACTCTTACACTGTGGGATCCCAGAAGATAAAC 3720
Qy  3721 TCAGTCAAGTCTACATTATTCTGTATGATGCGTGCAGAGAGTCTGTGTCGACTCTACAAGT 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 TCAGTCAAGTCTACATTATTCTGTATGATGCGTGCAGAGAGTCTGTGTCGACTCTACAAGT 3780
Qy  3781 TGGAAGCTAAATTTGTAATCGTCTTTGTCTTGCAAGATCTCTAATAGTCGTGTCAATAAATTCATTAATAAAAC 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 TGGAAGCTAAATTTGTAATCGTCTTTGTCTTGCAAGATCTCTAATAGTCGTGTCAACAATAAATTCATTAATAAAAAC 3840
Qy  3841 TTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAATAAATCTGCAT 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 TTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAATAAATCTGCAT 3900
Qy  3901 AGAAAACAGGTATTGCACAGTTGGTGAACGTTACAGGTCTTAAAAGACCTAGAGGAGGTTGTTG 3960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 AGAAAACAGGTATTGCACAGTTGGTGAACGTTACAGGTCTTAAAAGACCTAGAGGAGGTTGTTG 3960
Qy  3961 GACTGTTGAAGAAACTCGGCATCCAAGTACCGGTCGATCAATTTGGCTTGGTTCA 4020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 GACTGTTGAAGAAACTCGGCACACAAGTTACGGTCGATCAATTTGGCTTGGTTCA 4020
Qy  4021 AGGTGCAGCAGCACAATGGAATCATCTTCCCAGTTGTTGTGGCTTTCATCAAAAGCAAGCCAAAA 4080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021 AGGTGCAGCAGCACCAATGGAATCATCTTCCCAGTTGTTGTGGCTTTCATCAAAAGCAAGCCAAA 4080
Qy  4081 GGGCTGTACCTGAAAATCCTGCGAGCTGGAGGCAGCAGATGATGACCTGCTGATTCCCCAGTTTA 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081 GGGCTGTACCTGAAAATCCTGCGAGCTGGAGGCAGCAGATGATGACTTGCTGATTCCCCAGTTTA 4140
Qy  4141 GAGGGCCACAAGCTCTGGGGCCCAGTTCCCACTGGGTCAGCATAGCTATAGACA 4200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141 GAGGGCCACAAGCTCTGGGGCCCAGTTCCCACTGGGTCAGCATAGCTATAGACA 4200
Qy  4201 AGATATCTGCTCGTGTCCTCAACATGAGGAATCTGTTACAATAAGTCTTGTGACCTCC 4260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201 AGATATCTGCTCGTGTCCTCAACATGGAGGAATCTGTTACAATAAGTCTTGTGACCTCC 4260
Qy  4261 TGGTTGTAAGTGTTGGTTGTGTCAGATGTCTATGTCCAGGGCCATCAACCTACCCGAAAACTCT 4320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4261 TGGTTGTAAGTGTTGGTTGTGTCAGATGTCTATGTCCAGGGCCATCAACCTACCCGAAAACTCT 4320
Qy  4321 GGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCCAAGAGGAATTAC 4380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4321 GGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCCAAGAGGAATTAC 4380
Qy  4381 AAGAGTACTGCGAGAATCATGAAATCACCATGTGGCCCTTGTCTCTCGGAATAAAGAGGAA 4440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4381 AAGAGTACTGCGAGAATCATGAAATCACCATGTGGCCCTTGTCTCTCGGAATAAAGAGGAA 4440
Qy  4441 GCCATGTCAAGGTTAAGTCTTTCGAGAAGGCAGACAGAGAAGGCGTGTCTGGAGA 4500
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Db  4441 GCCATGTCAAGGTTAAGTCTTTCGAGAAGGCAGACAGAGAAGGCGTGTCTGGAGA 4500
Qy  4501 CTGAACTTGTGTGACCATGTACTGCGAGAAACTGAGGACTAAAGTCACTGATGAAGGAATG 4560
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Db  4501 CTGAACTTGTGTGACCATGTACTGCGAGAAACTGAGGACTAAAGTCACTGATGAAGGAATG 4560
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GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
; APPLICANT: GANDHI, Ameena R.; TRIBOULEY, Catherine M.
; APPLICANT: KEARNEY, Liam; GRIFFIN, Jennifer A.
; APPLICANT: NGUYEN, Danniel B.; BANDMAN, Olga
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.
; APPLICANT: WALIA, Narinder K.; YAO, Monique G.
; APPLICANT: PATTERSON, Chandra; BURRILL, John D.
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.
; APPLICANT: RECIPON, Shirley A.; LU, Yan
; APPLICANT: POLICKY, Jennifer L.; THORNTON, Michael B.
; APPLICANT: TANG, Y. Tom; HAFALIA, April J.A.
; APPLICANT: ELLIOTT, Vicki S.; BAUGHN, Mariah R.
; APPLICANT: WALSH, Roderick T.; RAMKUMAR, Jayalaxmi
; APPLICANT: BOROWSKY, Mark L.; AU-YOUNG, Janice K.
; APPLICANT: HILLMAN, Jennifer L.; GURURAJAN, Rajagopal

```
Query Match          94.4%;  Score 5217.8;  DB 15;  Length 5305;
Best Local Similarity 99.5%;  Pred. No. 0;
Matches 5267;  Conservative 0;  Mismatches 12;  Indels 12;  Gaps 3;

Qy   63 ATGGCTGGGGCCGTGGGGCCCCGGGGCGGCGGCCTCCGGAGAGCTACCCG 122
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGGCTGGGGCCGTGGGGCCCCGGGGCGGCGGCCTCCGGAGAGCTACCCG 60

Qy  123 CAACGACAGGACCACGAGCTACAGGGCCGTCCATCTACGGCGGCGACTTCCAAGAC 182
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CAACGACAGGACCACGAGCTACAGGGCCGTCCATCTACGGCGGCGACTTCCAAGAC 120

Qy  183 CTGCGGCCGCCGCGACGCGTTGCCGGACCGGTCAAAGAGCCCCTGAAATCAATTAGTTTGTAC 242
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CTGCGGCCGCCGCGACGCGTTGCCGGACCGGTCAAAGAGCCCCTGAAATCAATTAGTTTGTAC 180

Qy  243 CCTCAAGGCCTAACTGGTGAAGAAGTATGTAGGGTAAAATGCCCA 302
        |||||||||||||||||||||||||||||||||||||||||
Db  181 CCTCAAGGCCTAACTGGTGAAGAAGTATGTAGGGTAAAATGCCCA 240

Qy  303 CCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAATGCCAAAGGTCTATCAAAT 362
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAATGCCAAAGGTCTATCAAAT 300

Qy  363 GAAAGTGTCAATTTGTTAAATCTCGCCTAGAGAACTGGCCAAGAAACACTGTGGGGAG 422
```

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Qy 4561 GCAGAGAAGCTTCCGATAATCTGCAGTGCAAAATCTGAAGGGGTCATTTCTAATGCTT 4620
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Db 4561 GCAGAGAAGCTTCCGATAATCTGCAGTGCAAAATCTGAAGGGGTCATTTCTAATGCTT 4620

Qy 4621 CAGGTTTGTTGAAATCCATGGAGCAACAGTGTGTTCCCATTGTGAGTGTGCTAGCCCCGG 4680
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4621 CAGGTTTGTTGAAATCCATGGAGCAACAGTGTGTTCCCATTGTGAGTGTGCTAGCCCCGG 4680

Qy 4681 AGAAGCTGTCAGCCAGCACTAGGAGGCGCTATGAAAACTCAGGTACAAACTCGACTTCAGA 4740
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4681 AGAAGCTGTCAGCCAGCACTAGGAGGCGCTATGAAAACTCAGGTACAAACTCGACTTCAGA 4740

Qy 4741 CCTCCCTTGCCAACTTACATCAGAAAAACAGTGAAATTCTGGCTGTGGGATCTAC 4800
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Db 4741 CCTCCCTTGCCAACTTACATCAGAAAAACAGTGAAATTCTGGCTGTGGGATCTAC 4800

Qy 4801 CCAAAGAAACAATATTACAGTTTTATCATTAGAGTGGGATGCTGATGAACAGGCATTTA 4860
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4801 CCAAAGAAACAATATTACAGTTTTATCATTAGAGTGGGATGCTGATGAACAGGCATTTA 4860

Qy 4861 ACACAACTGTGAAGCAGCTGCGTGTCACGCGTGCTGTGCTATTTCTGTACAGCT 4920
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4861 ACACAACTGTGAAGCAGCTGCGTGTCACGCGTGCTGTGCTATTTCTGTACAGCT 4920

Qy 4921 GTGATGAAATTTATACATCAAAGTAGAAAAAAGGTGTCTGTGCTATTTCTGTACAGCT 4980
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Db 4921 GTGATGAAATTTATACATCAAAGTAGAAAAAAGGTGTCTGTGCTATTTCTGTACAGCT 4980

Qy 4981 ATAGAGATGACTACTACACAGAATCTATTTTAACCCTAAAGAACGTGTCTTAACCTCATTC 5040
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4981 ATAGAGATGACTACTACACAGAATCTATTTTAACCCTAAAGAACGTGTCTTAACCTCATTC 5040

Qy 5041 AAACAGCAGCAGAGGCTTATACTGGAATAATGGAATGTGTACATTCATCATAATTTAAAAT 5100
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5041 AAACAGCAGCAGAGGCTTATACTGGAATAATGGAATGTGTACATTCATCATAATTTAAAAT 5100

Qy 5101 TAAATTCTAAGAAGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCACCACTTTGGGAA 5160
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5101 TAAATTCTAAGAAGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCACCACTTTGGGAA 5160

Qy 5161 GCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCCTGAGCAACAAAGCAA 5220
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5161 GCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCCTGAGCAACAAAGCAA 5220

Qy 5221 GACCCCATCTCTATAAAAACTAAAAAAAAATTAGTTGGGCATGGTGGCACATGCCTGTAGTC 5280
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5221 GACCCCATCTCTATAAAAACTAAAAAAAAATTAGTTGGGCATGGTGGCACATGCCTGTAGTC 5280

Qy 5281 CCAGCTACTCCAGAGGCTGAGATGGATCATCTCAGAGGTTGAGGCTGCAGTGA 5340
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5281 CCAGCTACTCCAGAGGCTGAGATGGATCATCTCAGAGGTTGAGGCTGCAGTGA 5340

Qy 5341 GCTGTGACTGCGCGCCACTGCACTCCAGTCTGGGCAACAAGAGCAAGACCCTGTCTTAAAAA 5400
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5341 GCTGTGACTGCGCGCCACTGCACTCCAGTCTGGGCAACAAGAGCAAGACCCTGTCTTAAAAA 5400

Qy 5401 AAAAAGAGAAAAAAAAATTTTTTTTTCTAAGAAGCTGTCTACAAAGTTGAGCTTTGTTAGT 5460
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 5401 AAAAAGAGAAAAAAAAATTTTTTTTTCTAAGAAGCTGTCTACAAAGTTGAGCTTTGTTAGT 5460

Qy 5461 TTTTCATGTGTAATATATTATTATAAAATTTATCTTTTGGGATATAATAAATGCTTCATATAC 5520
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5461 TTTTCATGTGTAATATATTATTATAAAATTTATCTTTTGGGATATAATAAATGCTTCATATAC 5520

Qy 5521 CTGCA 5525
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Db 5521 CTGCA 5525
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RESULT 2
US-10-258-106-33
; Sequence 33, Application US/10258106
; Publication No. US2004018185A1

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Db  1381 GTGTTGAGCAAACCCGAGTTCGTTTTAGTGACAATGCTCTGCCTTATAAAACGGGGAAG 1440
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Qy  1494 AAAGGAGATGTTTGGCGTCCTTGGCGTCGTGCTGCTGCTGCCTTCAGCCAAGCAGAGAATGT 1553
         ||||||| ||||||||||||||||||||||||| ||||||||| |||||||||||||||||
Db  1441 AAAGGAGATGTTTGGCGTCCTTGGCGTCGTGCCTTCGTGCTGCCTCAGCCAAGCAGCAGAATGT 1500

Qy  1554 GGAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACATTTCTAAAG 1613
         ||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  1501 GGAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCTAAAG 1560

Qy  1614 AAATGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTTGAAAACACAGC 1673
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 ---TGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTTGAAAACACAGC 1617

Qy  1674 TTTATAAATCCCAGCCAAAAATGCCCTAGTGGACAAAGTCCTGAAGATTCTGAAGGA 1733
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Qy  1734 CAAGATTATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGCCTTCTTTAGT 1793
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Db  1678 CAAGATTATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGCCTTCTTTAGT 1737

Qy  1794 GAGACACAGAGACAGTTTTCCCGATACTTCATTGAGTTTGAAGAATTACAACTTCTTGGT 1853
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1738 GAGACACAGAGACAGTTTTCCCGATACTTCATTGAGTTTGAAGAATTACAACTTCTTGGT 1797

Qy  1854 AAAGGAGCTTTTGGACTGTCATCAAGTGCAGAACAAGTTGACAAGTTGGACGGCTGCTACGCA 1913
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1798 AAAGGAGCTTTTGGACTGTCATCAAGTGCAGAACAAGTTGACAAGTTGGACGGCTGCTACGCA 1857

Qy  1914 GTGAAGCCGCATCCCATCAACCGGCCAGTTCCGCAGGATCAAGGGCGAAGTG 1973
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1858 GTGAAGCCGCATCCCATCAACCGGCCAGTTCCGCAGGATCAAGGGCGAAGTG 1917

Qy  1974 ACACTGCTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGCCTGGATCGAG 2033
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1918 ACACTGCTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGCCTGGATCGAG 1977

Qy  2034 CGGCACGAGCGGCCGGCCGGCGGCAGCTCCGGCAGCTCCGGCGGCCCCTGGCCAAG 2093
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Db  1978 CGGCACGAGCGGCCGGCCGGCGGCAGCTCCGGCAGCTCCGGCGGCCCCTGGCCAAG 2037

Qy  2094 GATGACCGAGCTGCACGCGGCAGCGCCGGCGAGCTCGGTGGAGTGGCACTTCGGGCGAGCGGC 2153
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2038 GATGACCGAGCTGCACGCGGCAGCGCCGGCGAGCTCGGTGGAGTGGCACTTCGGGCGAGCGGC 2097

Qy  2154 GCCGGCGGCGCCGCCATCCTCAGCAGCTCCGCCGCCACCGCCTCGGCGGACTCCCAGCAGAGCGAC 2213
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Db  2098 GCCGGCGGCGCCGCCATCCCATCCTCAGCAGCTCCGCCGCCACCGCCTCGGCGGACTCCCAGCAGAGCGAC 2157

Qy  2214 TCGGCCAGTGCCGTTCCCGCCCGTTCCCGGGCTCCAGCAGGGCTCCAGCGGACGATGACGAGGACGACGAC 2273
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Db  2158 TCGGCCAGTGCCCGTTCCCGGGCTCCAGCAGGGCTCCAGCATGACGATGACGACGACGAC 2217

Qy  2274 GAGGACGAGCGAGCAGCGGTGGTGGGCACGGTGGGCGTCTTCCTGCCGCTTCAGAATTCTGAAAGT 2333
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2218 GAGGACGAGCGAGCAGCGGTGGTGGGCACGGTGGGCGTCTTCTCCAGTCCTGCCGCTTCAGAATTCTGAAAGT 2277

Qy  2334 GATATTATCTTTGACAATGGCTGCCATGAGCAATCAGTAAAGTCAGTGCCATCAGTGACGACTGGCTGTGCACTAC 2393
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2278 GATATTATCTTTGACAATGGCTGCCATGAGCAATCAGTAAAGTCAGTGAGGCTGTGACTAC 2337

Qy  2394 AATGAAAAGAAATGGCTGCCATGAAAGTGAGACGACTGGCCATCAGTGAGGCTGTGCACTAC 2453
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2338 AATGAAAAGAAATGGCTGCCATGAAAGTGAGACGACTGGCCATCAGTGAGGCTGTGCACTAC 2397

Qy  2454 CTATACATCCAGATGGAGTACTGTGAGAAGAGACACCATTGACGACCAGGGA 2513
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Db  2398 CTATACATCCAGATGGAGTACTGTGAGAAGAGACACCATTGACGACCAGGGA 2457

Qy  2514 CTGTATCGAGACACCGTCAGACTCCGGAGGCTTTTCGGAGATTCTGGATGATTAGCT 2573
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2458 CTGTATCGAGACACCGTCAGACTCCGGAGGCTTTTCGGAGATTCTGGATGATTAGCT 2517
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Db   301 GAAAGTGTCAATTTGTTAAAATCTCGGCCTAGAGAACACTGTGGGGAG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||

Qy   423 GTGATGGATCTTTGAACTGGCTTACCACGTGCAGTCAGTCATTTCTTCAGCGAGCATAACAGCCC 482
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTGATGGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCTTCAGCGAGCATAACAGCCC 420

Qy   483 CCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGCTCAGGAGGAGCAGCAGCAGAG 542
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGCTCAAGAGGAGCAACAGAGG 480

Qy   543 CTGTTGGAGG--CCAAGCGGAAAGAGAGCAG------GACCAAGTGAAATCCTGCAT 593
         ||||||||||||||||||||||      ||||||||||||||
Db   481 CTGTTGGAGGCCCAAGCGGAAAGAGAGCAGGAAAAGAGGACCAAGTGAAATCCTGCAT 540

Qy   594 GAGATTCAGAGAGGAAGGAGAGAGAGATAAAGAGAGAAAGAGAAAGAGAAATGGCTAAG 653
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GAGATTCAGAGAGGAAGGAGAGAGAGATAAAGAGAGAAAGAGAAAGAGAAATGGCTAAG 600

Qy   654 CAGGAACGTTTGGAAAATTGCTAGTTGTCAAACCAAGATCATACCTTCTAAGAAGGACCCA 713
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CAGGAACGTTTGGAAAATTGCTAGTTGTCAAACCAAGATCATACCTTCTAAGAAGGACCCA 660

Qy   714 GGAGGACACAGAGACGGCTGCCATTCTACATGGAGGCTCCTCCTGACTTTGTAGGAAATGGT 773
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GGAGGACACAGAGACAGGCTGCCATTCTACATGGAGGCTCCTCCTGACTTTGTAGGAAATGGT 720

Qy   774 AAACATCGGGCAAACTCCTCAGGAAGTCTAGGCGGAACGTCAGTATTCTGTATGTAAT 833
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAACATCGGGCAAACTCCTCAGGAAGTCTAGGCGAGAACGTCAGTATTCTGTATGTAAT 780

Qy   834 AGTGAAGATTCTCCTGGCTTCTGTGAAATTCTGTATTCAATAGGGAGTCCTGATCAG 893
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 AGTGAAGATTCTCCTGGCTTCTGTGAAATTCTGTATTCAATATGGGAGTCCTGATCAG 840

Qy   894 CTCATGGTGCACAAAGGGAAATGTATTGCAGTGAGTGAATGAACAACTTGAAAATTAGTCTAC 953
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CTCATGGTGCACAAAGGGAAATGTATTGGCAGTGAGTGAATGAACAACTTGAAAATTAGTCTAC 900

Qy   954 AATGCTTTGAAACAGCAGCCACTGGTTGTTGTCTTGTGTTGTGTTGTGAGTGGGTCCTTCAGTGG 1013
         |||||||||||||||||||||||||||||||||||||||||||
Db   901 AATGCTTTGAAACAGCAGCCACTGGTTGTTGTCTTGTGTTGTGAGTGGGTCCTTCAGTGG 960

Qy  1014 CAGAAAAAAATGGGTCCATTCCTTACCACAGTCAAGACAGAAGAGAAGATTGATAAGTGCAAA 1073
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CAGAAAAAAATGGGTCCATTCCTTACCACAGTCAAGAGAAAGAGAGAATTGATAAGTGCAAA 1020

Qy  1074 AAGCAGATTCAAGGAACAGAGAACAGAAATCAACTCACTGGTAAAATTGAGCCATCCAAAT 1133
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 AAGCAGATTCAAGGAACAGAGAACAGAAATCAACTCACTGGTAAAATTGAGCCATCCAAAT 1080

Qy  1134 GTAGTACGTACCTTGCAATGAATCTCAAAGACGCAAGACGACTCCATCGTGTGGACATT 1193
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 GTAGTACGTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATTGTGTGGACATT 1140

Qy  1194 TTAGTGGAGCACATTAGTGGGTCTCTGCTTCTCCGCACCCTGCACACCTGACCCCCATC 1253
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 TTAGTGGAGCACATTAGTGGGTCTCTGCTTCTCCGCACCCTGACCCCCATC 1200

Qy  1254 CCTGTGCATCAGCTTCGCAGGTACACAGCTTCAGCCTGTCAGGCCTTGATTATCTGCAC 1313
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 CCTGTGCATCAGCTTCGCAGGTACACAGCTTCAGCCTGTCAGGCCTTGATTATCTGCAC 1260

Qy  1314 AGCAATTCTGGGTGCATAAGGTCCTGAGTGCATCTAATGTCTTGGATGCAGAAGGC 1373
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 AGCAATTCTGTGGGTGCATAAGGTCCTGAGTGCATCTAATGTCTTGGATGCAGAAGGC 1320

Qy  1374 ACCGTCAAGATTACGGACTATAGCATTCTAAGCGCCTTCGACAACATTTGCAAGAGGAT 1433
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Db  1321 ACCGTCAAGATTACGGACTATAGCATTCTAAGCGCCTTCGACAACATTTGCAAGAGGAT 1380

Qy  1434 GTGTTGAGCAAACCCGAGTTCGTTTTAGTGACAATGCTCTGCCTTATAAAAACGGGGAAG 1493
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Right column:

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Qy  3654 ATTTATTTGAACCATACCATGTTATTGAAAGCAATACTCTTACACTGTGGGATCCCAGAA 3713
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Db  3598 ATTTATTTGAACCATACCATGTTATTGAAAGCAATACTCTTACACTGTGGGATCCCAGAA 3657

Qy  3714 GATAAACTCAGTCAACATTATTCGTATGATGCTGTGACAGAGAAGCTGACGAGG 3773
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3658 GATAAACTCAGTCAACATTATTCGTATGATGCTGTGACAGAGAAGCTGACGAGG 3717

Qy  3774 AGAGAAGTGGAGCTAAATTTGTAATCGTCTTGTCTTCTAATAGTGTGTGTGACTC 3833
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3718 AGAGAAGTGGAGCTAAATTTGTAATCGTCTTGTCTTCTAATAGTGTGTGTGACTC 3777

Qy  3834 TACAAGTTTATTGAACAGAAGGGAGATTGCAAGACTTATGCCAACAATAAATTCATTA 3893
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Db  3778 TACAAGTTTATTGAACAGAAGGGAGATTGCAAGACTTATGCCAACAATAAATTCATTA 3837

Qy  3894 ATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGACCTAGAGGAG 3953
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3838 ATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGACCTAGAGGAG 3897

Qy  3954 GTTGTTGGACTGTTGAAGAAACTCGGCATCAAGTACAGGTCTTGATCAATTGGGCTTG 4013
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3898 GTTGTTGGACTGTTGAAGAAACTCGGCATCAAGTACAGGTCTTGATCAATTGGGCTTG 3957

Qy  4014 GTTACAAGGTGCAGCACAATGGAATCATCTTCAGTTTGTGGCTTTCATCAAACGA 4073
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Db  3958 GTTTACAAGGTGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTTCATCAAACGA 4017

Qy  4074 AGGCAAAGGCGTACTGAAAATCCTCGCAGTGGAGGCAGATATGACCTGCTGATTCCC 4133
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4018 AGGCAAAGGCGTACCTGAAAATCCTCGCAGTGGAGGCAGATATGACCTGCTGATTCCC 4077

Qy  4134 CAGTTTAGAGGGCCACAAGCTCTGGGGCCCACTGCCATTGGGGTCAGCATAGCT 4193
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4078 CAGTTTAGAGGGCCACAAGCTCTGGGGCCCACTGCCATTGGGGTCAGCATAGCT 4137

Qy  4194 ATAGACAAGATATCTGCTGCTGTCCTGTCCTGTCCTCAACATGGAGAATCTGTTACAATAAGCTCTTGT 4253
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4138 ATAGACAAGATATCTGCTGCTGTCCTGTCCTCAACATGGAGAATCTGTTACAATAAGCTCTTGT 4197

Qy  4254 GACCTCCTGTTGTAAGTGTTGGTCAGATGTCTATGTCCAGGGCCATCAACCTAACCCAG 4313
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4198 GACCTCCTGTTGTAAGTGTTGGTCAGATGTCTATGTCCAGGGCCATCAACCTAACCCAG 4257

Qy  4314 AAACTCTGACAGCAGCATCACAGCAGAAATCATGTCACTGGTCACAGACTCCAAGAG 4373
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Db  4258 AAACTCTGGACAGCAGCATCACAGCAGAAATCATGTCACTGGTCACAGACTCCAAGAG 4317

Qy  4374 GAATTACAAGTACTGCAGTACTGCAGCAGTCAGAAACTCACCTATGTGGCCCTTGTCTCTGGATAAA 4433
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Db  4318 GAATTACAAGTACTGCAGTACTGCAGCAGTCAGAAACTCACCTATGTGGCCCTTGTCTCTGGATAAA 4377

Qy  4434 GAAGGAAGCCATGTCAAGGTTAAGTCTTCGAAGGCAGAAAGGCAGAGAGAAGCGTGTG 4493
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4378 GAAGGAAGCCATGTCAAGGTTAAGTCTTCGAGAAGGAAGGCAGAGAGAAGCGTGTG 4437

Qy  4494 CTGGGAGACTGAACTGTGAACTGTTGGACCCATGTACTGCAGAAGCTAAAGTCACTGATGAA 4553
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4438 CTGGGAGACTGAACTGTGAACTGTTGGACCCATGTACTGCAGAAGCTAAAGTCACTGATGAA 4497

Qy  4554 AGGAATGGCAGAGAAGCTTCCGATAATCTTCGAGTGCAAATCTGAAGGGGTCATTTTCT 4613
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4498 AGGAATGGCAGAGAAGCTTCCGATAATCTTCGAGTGCAAATCTGAAGGGGTCATTTTCT 4557

Qy  4614 AATGCTTCAGGTTGTTGTTGAAATCCATGGAGCAACAGTCGTTCCATTGTGAGTGTGCTA 4673
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4558 AATGCTTCAGGTTGTTGTTGAAATCCATGGAGCAACAGTCGTTCCATTGTGAGTGTGCTA 4617

Qy  4674 GCCCCCGGAGAGCGTGTCAGCCGACACTAGGAGGGCCTATGAAACTCAGTGAAAACTCGA 4733
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4618 GCCCCCGGAGAGCGTGTCAGCCGACACTAGGAGGGCCTATGAAACTCAGTGAAAACTCGA 4677

Qy  4734 CTTCAGACCTCCCTGCCAACTTACATCAGAAAAGCAGTGAAATTGAAATTCTGGCTGTG 4793
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Left column:

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Qy  2574 TATATCCATGAGAAAGGAATGATTCACCGGGATTTGAAGCCTGTCAACATTTTTTGGAT 2633
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Db  2518 TATATCCATGAGAAAGGAATGATTCACCGGGATTTGAAGCCTGTCAACATTTTTTGGAT 2577

Qy  2634 TCTGATGACCATGTGAAAATAGGTGATTTGGTTTGGCGACAGACCATCTAGCCTTTTCT 2693
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2578 TCTGATGACCATGTGAAAATAGTGATTTGGTTTGGCGACAGACCATCTAGCCTTTTCT 2637

Qy  2694 GCTGACGAAACAGACGATCAGACAGAGACTTGATTAAGTCAGACCCTTCAGGTCAC 2753
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Db  2638 GCTGACGAAACAGACGATCAGACAGAGACTTGATTAAGTCAGACCCTTCAGGTCAC 2697

Qy  2754 TTAACTGGGAGTGGTTGGCACTGCTCTCATGTAAGCCCAGAGGTCCAAGGAAGCCACCAAA 2813
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Db  2698 TTAACTGGGAGTGGTTGGCACTGCTCTCATGTAAGCCCAGAGGTCCAAGGAAGCCACCAAA 2757

Qy  2814 TCTGCATACACAACCAGAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTTTGAGATGTCC 2873
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Db  2758 TCTGCATACAACCAGAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTTTGAGATGTCC 2817

Qy  2874 TATCACCCCATGGTCACGGCTTCAGAAAGGATCTTGTTCTCAACCAACTCAGAGATCCC 2933
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2818 TATCACCCCATGGTCACGGCTTCAGAAAGGATCTTGTTCTCAACCAACTCAGAGATCCC 2877

Qy  2934 ACTTCGCCTAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCAAAGCAGAAATCAGTC 2993
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Db  2878 ACTTCGCCTAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCAAAGCAGAAATCAGTC 2937

Qy  2994 ATCTCCTGGCGTGTTGAAACCACGATCCAGCAAAACGGCCCACAGCCACAGAACTGCTCAAG 3053
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2938 ATCTCCTGGCGTGTTGAAACCACGATCCAGCAAAACGGCCCACAGCCACAGAACTGCTCAAG 2997

Qy  3054 AGTGAGCTGCTGCGCCCCACCCCAGATGGAGGAGTCGATGAGCTGCAGAGTGCTGCACCAC 3113
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2998 AGTGAGCTGCTGCGCCCCACCCCAGATGGAGGAGTCGATGAGCTGCAGAGTGCTGCACCAC 3057

Qy  3114 ACGCTGACCAACGTGGATGGGAAGGCCTACCGGCACCATGATGGCCCAGATCTTCTCGCAG 3173
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3058 ACGCTGACCAACGTGGATGGGAAGGCCTACCGGCACCATGATGGCCCAGATCTTCTCGCAG 3117

Qy  3174 CGCATCTCCCCTGCCATCGATTACACCTTGTGTACTCCACTCTGCTCCCCGAAGGGCAACTTCTCA 3233
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3118 CGCATCTCCCCTGCCATCGATTACACCTTGTGTACTCCACTCTGCTCCCCGAAGGGCAACTTCTCA 3177

Qy  3234 ATCCGTACAGCCAAGATGCAGCAGCAGTGTGTGTGAAACCATCATCCGGATCGTGTGCTTTCCTTTTGAC 3293
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3178 ATCCGTACAGCCAAGATGCAGCAGCAGTGTGTGTGAAACCATCATCCGGATCGTGTGCTTTCCTTTTGAC 3237

Qy  3294 CATGGAGCTGTTCAGTTGTGTACTCCACTTGGGCAAGAAACAGACAAAATATATGAG 3353
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3238 CATGGAGCTGTTCAGTTGTGTACTCCACTTGGGCAAGAAACAGACAAAATATATGAG 3297

Qy  3354 CACAACGAAGGTGCCCTATTCATGAGACCCACAGCCGGGATGCTGGTGATGCTTCCTTTTGAC 3413
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3298 CACAACGAAGGTGCCCTATTCATGAGACCCACAGCCGGGATGCTGGTGATGCTTCCTTTTGAC 3357

Qy  3414 CTGCGCGGATCCCTTTTGCAAGATGTGGCAAGAAATATAATATATTTAAAACGATAC 3473
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3358 CTGCGCGGATCCCTTTTGCAAGATGTGGCAAGAAATATAATATATTTAAAACGATAC 3417

Qy  3474 TGCATAGAACGTGTGTTCAGGGCCGCCCGCCCAAGTTAGATCGATTTCATCCCAAAGAAACTTCTG 3533
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3418 TGCATAGAACGTGTGTTCAGGGCCGCCCGCCCAAGTTAGATCGATTTCATCCCAAAGAAACTTCTG 3477

Qy  3534 GAGTGTGCATTTGATATTGTCACTTCACTCCACCACCAACAGTTTCTGCCCACTGCTGAAATT 3593
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3478 GAGTGTGCATTTGATATTGTCACTTCACTCCACCACCAACAGTTTCTGCCCACTGCTGAAATT 3537

Qy  3594 ATCTACTATCCTATGAAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAGAAATTACAGT 3653
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3538 ATCTACTATCCTATGAAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAGAAATTACAGT 3597
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Qy
Db

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Db   4678  |||||||||||||||||||||||||||||||||||||||||||||
           CTTCAGACCTCCCTTGCCAACTTACATCAGAAAAGCAGTGAAATTCTGGCTGTG  4737

Qy   4794  GATCTACCCAAAGAAAACAATATTACAGTTTTTATCATTAGAGTGGGATGCTGATGAACAG  4853
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4738  GATCTACCCAAAGAAAACAATATTACAGTTTTTATCATTAGAGTGGGATGCTGATGAACAG  4797

Qy   4854  GCATTAACACACTGTGAAGCAGTCTGCTGTCACGCCTGCCAAGCAAAGATAACCTCAAA  4913
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4798  GCATTTAACACACTGTGAAGCAGTCTGCTGTCACGCCTGCCAAGCAAAGATAACCTCAAA  4857

Qy   4914  TTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAAGGTGTCTGTGCTATTTCTG  4973
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4858  TTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAAGGTGTCTGTGCTATTTCTG  4917

Qy   4974  TACAGCTATAGAGATGACTACTACAGAGAATCTTATTTTAACCCTAAAGAACTGTCGTTAAC  5033
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4918  TACAGCTATAGAGATGACTACTACAGAGAATCTTATTTTAACCCTAAAGAACTGTCGTTAAC  4977

Qy   5034  CTCATTCAAACACAGACAGAGGCCTTATACTGGAATAATGGAATGTTGTACATTCATCATAAT  5093
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4978  CTCATTCAAACACAGACAGAGGCCTTATACTGGAATAATGGAATGTTGTACATTCATCATAAT  5037

Qy   5094  TTAAAATTAAATTCTAAGAAGAGAGGCTGGGTGCAGTGGCTCACACCTTAATCCCAGCACT  5153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5038  TTAAAATTAAATTCTAAGAAGAGAGGCTGGGTGCAGTGGCTCACACCTTTAATCCCAGCACT  5097

Qy   5154  TTGGGAAGCCAAGGCAGGAGGAAGACTTGCTTGAAACCAGGAGTTTGAGACCAGCCTGAGCAAC  5213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5098  TTGGGAAGCCAAGGCAGGAGGAAGACTTGCTTGAAACCAGGAGTTTGAGACCAGCCTGAGCAAC  5157

Qy   5214  AAAGCAAGACCCCATCTCTATAAAAACTAAAAAAATTAGTTGGGCATGGTGGCACATGCC  5273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5158  AAAGCAAGACCCCATCTCTATAAAAACTAAAAAAATTAGTTGGGCATGGTGGCACATGCC  5217

Qy   5274  TGTAGTCCCAGCTACTCCAGAGGCTGAGATGGATCATCTGAGCCTCAGGAGTTGAGGCT  5333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5218  TGTAGTCCCAGCTACTCCAGAGGGTGAGATGGATCATCTGAGCCTCAGGAGTTGAGGCT  5277

Qy   5334  GCAGTGAGCTG  5344
           |||||  |||||
Db   5278  GCAGTTAACTG  5288
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Query Match             91.2%;  Score 5040.8;  DB 12;  Length 5044;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 5042;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy     54  AGCGGCTGCCATGGCCATGGGCCGTGGGGGCCGTGGGGGCCCCGGGGCGCGCGGGACGAGCCTCCGGAG  113
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  AGCGGCTGCCATGGCCATGGGCCGTGGGGGCCGTGGGGGCCCCGGGGCGCGCGGGACGAGCCTCCGGAG   60

Qy    114  AGCTACCCGCAACGACACGAGCTACGGCGCGCGGAC  173
           |||||||||||||||||||||||||||||||||||
Db     61  AGCTACCCCGCAACGACACGAGCTACGGCGCGCGGAC  120

Qy    174  TTCCAAGACCTGCGCGCCGACGCTTGCGACCGGTCAAGAGCCCCTGAAATCAATTTA  233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  TTCCAAGACCTGCGCGCCGACGCTTGCGACCGGTCAAGAGCCCCTGAAATCAATTTA  180

Qy    234  GTTTTGTACCCTCAAGGCCTAACTGGTGAAGAGTATATGTAAAAATAGAGTTAAAAAATGCCAAAGT  293
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GTTTTGTACCCTCAAGGCCTAACTGGTGAAGAGTATATGTAAAAATAGAGTTAAAAAATGCCAAAGT  240

Qy    294  AAATGCCACCTACCTATCCAGATGTAGTTCCTAGAACTCGCCTAGAAGAACTGGCCAAGAAACAC  353
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  AAATGCCACCTACCTATCCAGATGTAGTTCCTAGAACTCGCCTAGAAGAACTGGCCAAGAAACAC  300

Qy    354  CTATCAAATGAAAGTGTCAATTTGTTAAAATCTTGTGGGGAGTGATGATCTTTGAACTGGCTTA  413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CTATCAAATGAAAGTGTCAATTTGTTAAAATCTTGTGGGGAGTGATGATCTTTGAACTGGCTTA  360

Qy    414  TGTGGGGAGTGATGATCTTTGAACTGGCTTA  473
           ||||||||||||||||||||||||||||||
Db    361  TGTGGGGAGTGATGATCTTTGAACTGGCTTA  420

Qy    474  AACAAGCCCCTCCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGCTCAGGAGGAG  533
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  AACAAGCCCCTCCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGCTCAGGAGGAG  480

Qy    534  CAGCAGAGGCTGTTGGAGGCCAAGCAAGGAGGAGCAACGTGAAATCCTGCAT  593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CAGCAGAGGCTGTTGGAGGCCAAGCAAGGAGGAGCAACGTGAAATCCTGCAT  540

Qy    594  GAGATTCAGAGAGGAAGGAAAGAAGAGATAAAAGAGGAAGAAAAAAGGAAAGAAATGGCTAAG  653
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GAGATTCAGAGAGGAAGGAAAGAAGAGATAAAAGAGGAAGAAAAAAGGAAAGAAATGGCTAAG  600

Qy    654  CAGGAACGTTTGGAAATTGCTAGTTTGTCAAACCAAGATCATACCTCTAAGGAGGACCCA  713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  CAGGAACGTTTGGAAATTGCTAGTTTGTCAAACCAAGATCATACCTCTAAGGAGGACCCA  660

Qy    714  GGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGTAGGAAATGGT  773
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  GGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGTAGGAAATGGT  720

Qy    774  AAACATGGGCAAACTCCTCAGGAGGTCTAGGCGGAGAACGTCAGTATTCTGTATGTAAT  833
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Db   1801  AAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGCAACAAGTTGGAGACGGCTGCTGCTACGCA  1860
           ||||||||||||||||||||||||
Qy   1914  GTGAAGAGGCCATCCCATCAACCGGCCAGTCCGCAGGATCAAGGGCGAAGTG  1973
           ||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1861  GTGAAGAGGCGATCCCATCAACCCGGCCAGTCCGCAGGATCAAGGGCGAAGTG  1920

Qy   1974  ACACTGCTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACACGCCTGATCGAG  2033
           ||||||||||||||||||||||||||||| ||||||||||||||| ||||||||||||
Db   1921  ACACTGCTGTCACGGCTGCACCATGAGAACACATTGTGCGCTACTACAACGCCTGATCGAG  1980

Db   2034  CGGCAGCAGACGGCGGCCGGCGGCCGGGGACGCGGCCGCCCGACTCCGGGCCCCTGCCCAAG  2093
           |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   1981  CGGCAGCAGACGGCGGCCGGCGGCCGGGGACGCGGCCGCCCGACTCCGGGCCCCTGCCCAAG  2040

Qy   2094  GATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGGCCGGCCTGGACACGGCTTGGACAGCGAGAG  2153
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  GATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGGCCGGCCTGGACACGGCTTGGACAGCGTAGAG  2100

Qy   2154  GCCGCGGCCGCCACCATCCTCAGCAGTCGCGGGCTCCAGCGACGATCGGAGCACTTCGGGCGAGCGC  2213
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  GCCCGCGGCCGCCACCCATCCTCAGCAGTCGCGGGCTCCAGCGACGATCGGAGCACTTCGGGCGAGCGC  2160

Qy   2214  TCGGCCAGTGCCCGTTTCCCGGCCCACCGGCTCCAGCGATGACGAGCACGACGAC  2273
           ||||||||||||||| ||||| ||||||||||||||||||||||||||||||||||
Db   2161  TCGGCCAGTGCCCGTTTCCCGGCCCACCGGCTCCAGCGATGACGAGCACGACGAC  2220

Qy   2274  GAGGACGAGCACGCGGTGGGGTCTTCTCCGCTGCTCCTGCCTTCCTGCTTCTCAGATTCTGAAAGT  2333
           ||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   2221  GAGGACGAGCACGCGGTGGGGTCTTCTCCCAGTCCTGCCTTCCTGCTTCTCAGATTCTGAAAAGT  2280

Qy   2334  GATATTATCTTTGACAATGAGATGAGAACAGTAAAAGTCAGAATCAGGATGAAGATTGC  2393
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   2281  GATATTATCTTTGACAATGAAGATGAGAACAGTAAAAGTCAGAATCAGGATGAAGATTGC  2340

Qy   2394  AATGAAAAAGAATGGCTGCCATGAGAACTAGTGTGAGAGAGAGCACTTTACGAGACACCATTGACCACGGGA  2453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  AATGAAAAAGAATGGCTGCCATGAGAACTAGTGTGAGAGAGAGCACTTTACGAGACACCATTGACCACGGGA  2400

Qy   2454  CTATACATCCAGATGAGACTGTGAGAAGATCTGAGACTCGAGAGGCTTTTCGAGATGATTAGCT  2513
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  CTATACATCCAGATGAGACTGTGAGAAGATCTGAGACTCGAGAGATTCTGAGAGATGATTAGCT  2460

Db   2514  CTGTATCGACACACCGTCAGACTCTGAGATTCTGGCTTTTCGAGATTCTGCAACATTTTTTTGAT  2573
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  CTGTATCGACACACCGTCAGACTCTGGAGCGCTTCTGGAGAGATTCTGGAGAGATTCTGCAACATTTTTTTGGAT  2520

Qy   2574  TATATCCATGAGAAAGGAATGATTCACCGGGATTTGAGAGCCTGTCAACATTTTTTTGAT  2633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  TATATCCATGAGAAAGGAATGATTCACCGGGATTTGAGAGCCTGTCAACATTTTTTTGAT  2580

Qy   2634  TCTGATGACCATGTGAAAATAGTGATTTGGTTTGGCGACAGGACCATCTAGCCTTTTCT  2693
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  TCTGATGACCATGTGAAAATAGGTGATTTGGTTTGGGCACAGGACCATCTAGCCTTTTCT  2640

Qy   2694  GCTGACAGCAAACAAGACGATCAGACAGGATCTTGTTCTGCAAAGAGATCTTGTCAACAGTGCCTGGAAGCACCAAA  2753
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  GCTGACAGCAAACAAGACGATCAGACAGGATCTTGTTCTGCAAAGAGATCTTGTCAACAGTGCCTGGAAGCACCAAA  2700

Qy   2754  TTAACTGGGATGGTTGGCACTGGGAAATGGCCTAGTGGAACAAAGTCCTGGAACAAAATTTCTAAAG  2813
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  TTAACTGGGATGGTTGGCACTGGGAAATGGCCTAGTGGAACAAAGTCCTGGAACAAAATTTCT  2760

Qy   2814  TCTGCATAACCAGAAGTGGATCTCTTCAGCCTGGATAATTATCTTCTTGAGATGTCC  2873
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  TCTGCATAACCAGAAGTGGATCTCTTCAGCCTGGGATAATTATCTTCTTGAGATGTCC  2820

Qy   2874  TATCACCCCATGGTCACGGCTTCAGAAGGATCTTTGTTCTCAACCAACTCAGATCCC  2933
           ||||| |||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   2821  TATCCCCCCATGGTCACGGCTTCAGAAGGATCTTTGTTCTCAACCAACTCAGATCCC  2880

Qy   2934  ACTTCGCCTAAGTTTCCAGAGACTTTGACGGCTGCTGCTACGGC  2993
           |||||||||||||||||||||||||||||||||||||||||||
Db   2881  ACTTCGCCTAAGTTTCCAGAGACTTTGACGGCTGCTGCTACGGC  2940
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Db    721  AAACATCGGGCAAACTCCTCAGGAAGGTCTAGGCGAGAACGTCAGTATTCTGTATGTAAT  780
           ||||||||||||||||||||||||
Qy    834  AGTGAAGAGATTCTCCTGGCCTTCTTGTGAAATTCTGTATTCAATATGGGAGTCCTGATCAG  893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  AGTGAAGAGATTCTCCTGGCCTTCTTGTGAAATTCTGTATTCAATATGGGAGTCCTGATCAG  840

Qy    894  CTCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACTTGAAAAATTAGTCTAC  953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CTCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACTTGAAAAATTAGTCTAC  900

Qy    954  AATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTTGTGTATGAGTGGTCCTTCAGTGG  1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  AATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTTGTGTATGAGTGGTCCTTCAGTGG  960

Qy   1014  CAGAAAAAAATGGTCCATTCCTTACCCAGTCAAGAAAAGAAGAAGAGATTGATAAGTGCAAA  1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  CAGAAAAAAATGGTCCATTCCTTACCCAGTCAAGAAAAGAAGAAGAGATTGATAAGTGCAAA  1020

Qy   1074  AAGCAGATTCAAGGAACAGAAACAGAATCAACTCACTGGTAAAAATTGAGCCATCCAAAT  1133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  AAGCAGATTCAAGGAACAGAAACAGAATCAACTCACTGGTAAAAATTGAGCCATCCAAAT  1080

Qy   1134  GTAGTACGCTACCTTGCAATGAATCTCAAAGACGAACATTCCATCGTGTGGTGGACATT  1193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  GTAGTACGCTACCTTGCAATGAATCTCAAAGACGAACATTCCATCGTGTGGTGGACATT  1140

Qy   1194  TTAGTGGAGCACATTAGTGGGTCTCTCTTGCTCCACACCTCAGCCCCATC  1253
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TTAGTGGAGCACATTAGTGGGTCTCTCTTGCTCCACACCTCAGCCCCATC  1200

Qy   1254  CCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTCAGGCCTTCGGTGCGATCGAGAGGC  1313
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTCAGGCCTTCGGTGCGATCGAGAGGC  1260

Db   1314  AGCAATTCTGTGGTGGTCATAAGGTCCTGAGTGCATCTAATGTCTTGGTGGTGCAGAAGGC  1373
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  AGCAATTCTGTGGTGGTCATAAGGTCCTGAGTGCATCTAATGTCTTGGTGGTGCAGAAGGC  1320

Qy   1374  ACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTTCGCAGACATTTGCAAGGAGGAT  1433
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTTCGCAGACATTTGCAAGGACGAT  1380

Db   1434  GTGTTTGAGCAAACCCGAGTTCGTTTAGTGACAAGTGCTCGCCTTATAAAACGGGGAAG  1493
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  GTGTTTGAGCAAACCCGAGTTCGTTTAGTGACAAGTGCTCGCCTTATAAAACGGGGAAG  1440

Qy   1494  AAAGGAGATGTTTGGCGTCCCTTCTGTCCCCTCAGCCAAGGACAGCAGAATGT  1553
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  AAAGGAGATGTTTGGCGTCCCTTCTGTCCCCTCAGCCAAGGACAGCAGAATGT  1500

Qy   1554  GGAGAGTACCCTGTGACCATCCCAGTGACTTACCAGCTGTCCCCAGACTTTCAAGAGATTTCTAAAG  1613
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  GGAGAGTACCCTGTGACCATCCCAGTGACTTACCAGCTGTCCCCAGACTTTCAAGAGATTTCTAAAG  1560

Qy   1614  AAATGTGTGTGCTTGATGACAGAAGGAGAAATGAGTCCCCAGCAGTTGTTGAAACACAGC  1673
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  AAATGTGTGTGCTTGATGACAGAAGGAGAAATGAGTCCCCAGCAGTTGTTGAAACACAGC  1620

Qy   1674  TTTATAAATCCCCAGCCAAAAATGCCTCAGTGAACAAAGGCTGACTTTCAAGATTTTCTAAAG  1733
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  TTTATAAATCCCCAGCCAAAAATGCCTCAGTGAACAAAGGCTGACTTTCAAGATTTTCTAAAG  1680

Qy   1734  CAAGATTATGTTGAGACTAGTTTATTCCTAGACAACCGGCTACCCAGTGCTGCCTTCTTTAGT  1793
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  CAAGATTATGTTGAGACTAGTTTATTCCTAGACAACCGGCTACCCAGTGCTGCCTTCTTTAGT  1740

Qy   1794  GAGACACAGAGACAGTTTCCCGATACTTCATTGAGTTTGAAGAATTACAACTTCTTGGT  1853
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  GAGACACAGAGACAGTTTCCCGATACTTCATTGAGTTTGAAGAATTACAACTTCTTGGT  1800

Qy   1854  AAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGCAACAAGTTGGACGGCTGCTGCTACGCA  1913
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 4074 AGGCAAAGGGCTGTACCTGGTGTGAAATCCTGAAATCCTGCAGCTGGAGGCAGATATGATGACCTGCTGATTCCC 4133
Db 4021 AGGCAAAGGGCTGTACCTGGTGTGAAATCCTGAAATCCTGCAGCTGGAGGCAGATATGACCTGCTGATTCCC 4080

Qy 4134 CAGTTTAGAGGGCCACAAGCTCTGGGGCCCAGTTCCCACTGCTGCCACTGCTCAGCATAGCT 4193
Db 4081 CAGTTTAGAGGGCCACAAGCTCTGGGGCCCAGTTCCCACTGCTGCCACTGCTCAGCATAGCT 4140

Qy 4194 ATAGACAAGATATCTGCTGCTGCCTCAACATGGAGAATCTGTTACAATAAGCTCTTGT 4253
Db 4141 ATAGACAAGATATCTGCTGCTGCCTCAACATGGAGAATCTGTTACAATAAGCTCTTGT 4200

Qy 4254 GACCTCCTGTTGTAAGTGTTGGTCAGATGTCTATGTCCAGGGCCATCAACCTAACCCAG 4313
Db 4201 GACCTCCTGTTGTAAGTGTTGGTCAGATGTCTATGTCCAGGGCCATCAACCTAACCCAG 4260

Qy 4314 AAACTCTGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCCCAAGAG 4373
Db 4261 AAACTCTGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCCCAAGAG 4320

Qy 4374 GAATACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGTCCCGGATAAA 4433
Db 4321 GAATACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGTCCCGGATAAA 4380

Qy 4434 GAAGGAAGCCATGTCAAGGTAAGTCTTTCGAGAAGAGAAAGGCAGACAGAAGCGTGTG 4493
Db 4381 GAAGGAAGCCATGTCAAGGTAAGTCTTTCGAGAAGAGAAAGGCAGACAGAAGCGTGTG 4440

Qy 4494 CTGGAGACTGAACTTGTGACCATGTACTGCAGAAATCTGAGACTCACTGATGAA 4553
Db 4441 CTGGAGACTGAACTTGTGACCATGTACTGCAGAAATCTGAGACTCACTGATGAA 4500

Qy 4554 AGGAATGGCAGAGAGCTTCCGATAATCTTCGAGTGCAAAATCTGAAGGGGTCATTTTCT 4613
Db 4501 AGGAATGGCAGAGAGCTTCCGATAATCTTCGAGTGCAAAATCTGAAGGGGTCATTTTCT 4560

Qy 4614 AATGTTCAGGTTGTTGTTGAAATCCATGGAGCAACAGTGGTTCCATTGTGAGTGTGCTA 4673
Db 4561 AATGTTCAGGTTGTTGTTGAAATCCATGGAGCAACAGTGGTTCCATTGTGAGTGTGCTA 4620

Qy 4674 GCCCCGGAGAAGCTGTCAGCCAGCACTAGGAGGCGCTATGAAAACTCAGTACAAAACTCGA 4733
Db 4621 GCCCCGGAGAAGCTGTCAGCCAGCACTAGGAGGCGCTATGAAAACTCAGTACAAAACTCGA 4680

Qy 4734 CTTCAGACCTCCCTGCCAACTTACACATACAGTTTTATCATTAGAGTGCTGATGAACAG 4793
Db 4681 CTTCAGACCTCCCTGCCAACTTACACATACAGTTTTATCATTAGAGTGCTGATGAACAG 4740

Qy 4794 GATCTACCCAAAGAACAATATTACAGTTTATCATTAGAGTGGGATGCTGATGAACAG 4853
Db 4741 GATCTACCCAAAGAACAATATTACAGTTTATCATTAGAGTGGGATGCTGATGAACAG 4800

Qy 4854 GCATTTAACACAACTGAGAGCAGCTGCTAAAGATACCTCAAA 4913
Db 4801 GCATTTAACACAACTGAGAGCAGCTGCTAAAGCAAAGATACCTCAAA 4860

Qy 4914 TTAGTCTGTGATGAAATTTATAACATCAAAGTAATGGAATATGTGTCATCATCATATAT 4973
Db 4861 TTAGTCTGTGATGAAATTTATAACATCAAAGTAATGGAATATGTGTACATCATCATATAT 4920

Qy 4974 TACAGCTATAGATGACTACTACAGAAATCTTATTTTAACCCTAAAGAACTGTCGTTAAC 5033
Db 4921 TACAGCTATAGATGACTACTACAGAAATCTTATTTTAACCCTAAAGAACTGTCGTTAAC 4980

Qy 5034 CTCATTCAAACAGCAGAGAGCTTATACTGAATAATGACGTTATCATTCATCATATAT 5093
Db 4981 CTCATTCAAACAGCAGAGAGCTTATACTGAATAATGACTGAATAATGTTGTACATCATCATATAT 5040

Qy 5094 TTAA 5097
Db 5041 TTAA 5044

Qy 2994 ATCCTCGGCTGTGTGAACCGATCCAGCAAACGGCCCACGAGCCTGCTCAAG 3053
Db 2941 ATCCTCGGCTGTGTGAACCAGGATCCAGCAAAACGGCCCACAGCCCAGAGCTGCTCAAG 3000

Qy 3054 AGTGAGCTGCTGCCCCCAACCCCCAGATGAGGGAGCTCAGAGCTCAGAGTGAAGTGCTGCGACCAC 3113
Db 3001 AGTGAGCTGCTGCCCCCAACCCCCAGATGAGGGAGCTCAGAGCTGCAGAGTGCTGCGACCAC 3060

Qy 3114 ACGCTGACCAACGTGGATGGAAGGCCTACCGCACCATGATGGCCCATCTTCTCGCAG 3173
Db 3061 ACGCTGACCAACGTGGATGGAAGGCCTACCGCACCATGATGGCCCATCTTCTCGCAG 3120

Qy 3174 CGCATCTCCCTGCCATGAGATTACACCTATGACAGCGACATACTGAAGGGCAACTTCTCA 3233
Db 3121 CGCATCTCCCTGCCATGAGATTACACCTATGACAGCGACATACTGAAGGGCAACTTCTCA 3180

Qy 3234 ATCCGTACAGCCAAGATGAGCAGCATGTGTGTGAAACCATCATCCGCATCTTTAAAAGA 3293
Db 3181 ATCCGTACAGCCAAGATGAGCAGCATGTGTGTGAAACCATCATCCGCATCTTTAAAAGA 3240

Qy 3294 CATGGAGCTGTTCAGTTGTACTGCTCCACTACTGCTTCCCGAAACAGACAAATATATGAG 3353
Db 3241 CATGGAGCTGTTCAGTTGTACTGCTCCACTACTGCTTCCCGAAACAGACAAATATATGAG 3300

Qy 3354 CACAACGAAGCTGCCCTATTCATGGACCACCAGCGGATGCTGTGATGCTTCCTTTTGAC 3413
Db 3301 CACAACGAAGCTGCCCTATTCATGGACCACCAGCGGATGCTGTGATGCTTCCTTTTTGAC 3360

Qy 3414 CTGCGGGATCCCTTTGCAAGAGATAATGTGGCAAGAAATAATAATAATTGAATTAAAACGATAC 3473
Db 3361 CTGCGGGATCCCTTTGCAAGAGATGTGGCAAGAAATAATAATAATTGAATTAAAACGATAC 3420

Qy 3474 TGCATAGAACGTGTGTCAGGCCGGCCAGTGAAGTTAGATCGAGTTTCATCCCAAAGAACTTCTG 3533
Db 3421 TGCATAGAACGTGTGTCAGGCCGGCCAGTGAAGTTAGATCGAGTTTCATCCCAAAGAACTTCTG 3480

Qy 3534 GAGTGTGCATTTGATATTGTCACTTCTCTACCACCAACAGCTTTCTGCCCACTGCTGAAATT 3593
Db 3481 GAGTGTGCATTTGATATTGTCACTTCTCTACCACCAACAGCTTTCTGCCCACTGCTGAAATT 3540

Qy 3594 ATCTACCATCTATGAAAATCATCCAAGAGTTCCAGCACTCAGGAAGAAATTACAGT 3653
Db 3541 ATCTACCACTATCTATGAAAATCATCCAAGAGTTCCAGCACTCAGGAAGAAATTACAGT 3600

Qy 3654 ATTTATTTGAACCATACCATGTATTGTAATGCAATTACTCTTACACTCTTCATCCCAGAA 3713
Db 3601 ATTTATTTGAACCATACCATGTATTGTAATGCAATTACTCTTACACTCTTCATCCCAGAA 3660

Qy 3714 GATAAAACTCAGTCAAGTCGCAGTTCGTGTATATCTGTATGATGCTCACATTGTGACAGCTGTGTGTGGACGAGG 3773
Db 3661 GATAAAACTCAGTCAAGTCGCAGTTCGTGTATATCTGTATGATGCTCACATTGTGACAGCTGTGTGTGGACGAGG 3720

Qy 3774 AGAGAAGTGGAAGCTAAATTTGTAATCTGTCTTTGTCTTCTAATAGTCTGTGTGTGACTC 3833
Db 3721 AGAGAAGTGGAAGCTAAATTTGTAATCTGTCTTTGTCTTCTAATAGTCTGTGTGTGACTC 3780

Qy 3834 TACAAGTTTATTGAACAGAGGGAGATTTGCAAGATCTTATGCCAACAATAAATTCATTA 3893
Db 3781 TACAAGTTTATTGAACAGAGGGAGATTTGCAAGATCTTATGCCAACAATAAATTCATTA 3840

Qy 3894 ATAAAACAGAAAACAGGTAATTGCACAGTTGCACGAGTATGCATTAAAGACCTAGAGAG 3953
Db 3841 ATAAAACAGAAAACAGGTAATTGCACAGTTGCACGAGTATGCATTAAAGACCTAGAGAG 3900

Qy 3954 GTTGTTGGACTGTTGAAGAAACTCGGCATCGCCAAGGTTACAGGTCTTGATCAATTTGGGCTTG 4013
Db 3901 GTTGTTGGACTGTTGAAGAAACTCGGCATCGCCAAGGTTACAGGTCTTGATCAATTTGGGCTTG 3960

Qy 4014 GTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTTGGCTTTCATCAAACCGA 4073
Db 3961 GTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTTGGCTTTCATCAAACCGA 4020

RESULT 4
US-10-174-333-138
; Sequence 138, Application US/10174333
; Publication No. US20040029220A1
GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grosse, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: CuraSeqList version 0.1
;
; SEQ ID NO 138
; LENGTH: 5094
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(4897)
US-10-174-333-138

Query Match   90.6%;   Score 5005.2;   DB 12; Length 5094;
Best Local Similarity   98.6%;   Pred. No. 0;
Matches 5086;   Conservative   0;   Mismatches   3; Indels   69; Gaps   1;

Qy   49 GGCGCAGCGCTGCCATGGCGTGGGGCCGTGGGGGCCGGCCCCCGGCGCGCGGGGGACGAGCCTC 108
            ||||||||||||||||||||||||||||||||||| |||||||| |||||||||||||||
Db   6 GGCGCAGCGCTGCCATGGCGTGGGGCCGTGGGGGCCGTGGGGCGCGGCGCCCGGGGACGAGCCTC 65

Qy   109 CGGAGGAGCTACCGCCAACGACAGGAGCACCAGCTACAGGCGCTACAGGCCCTGAGGCCATCTACGGCG 168
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 CGGAGGAGCTACCGCCAACGACAGGAGCACCAGCTACAGGCGCTACAGGCCCTGAGGCCATCTACGGCG 125

Qy   169 CGGACTTCCAAGACCTTGCGGACGCCGGACCGGTCAAAGAGCCCCTGAAATCA 228
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 CGGACTTCCAAGACCTTGCGGACGCCGGACCGGTCAAAGAGCCCCTGAAATCA 185

Qy   229 ATTTAGTTTGTACCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAGTGGATTTGA 288
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   186 ATTTAGTTTGTACCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGATTTGA 245

Qy   289 GGGTTAAATGCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTAAAAATGCCA 348
            |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   246 GGGTTAAATGCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTAAAAAATGCCA 305

Qy   349 AAGGTCTATCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAGAGAACTGGCCAAGA 408
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 AAGGTCTATCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAGAGAACTGGCCAAGA 365

Qy   409 AACACTGTGGGGAGTGATGATCTTGAACTGGCTTACCACGTGCAGTCATTTCTCAGCG 468
            ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 AACACTGTGGGGAGGTGATGATCTTGAACTGGCTTACCACGTGCAGTCATTTCTCAGCG 425

Qy   469 AGCATAACAAGCACCCCTCCCAAGTCTTTTCATGAAGAAAATGCTGGAAAGGCGGGCTCAGG 528
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 AGCATAACAAGCACCCCTCCCAAGTCTTTTCATGAAGAAAATGCTGGAAAGGCGGGCTCAGG 485

Qy   529 AGGAGCAGCAGAGGCTGTTGGAGCCAAGCGGAAAAGAGAGAGCAGCAGCAACGTGAAATCC 588
            ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   486 AGGAGCAGCAGAGGCTGTTGGAGCCAAGCGGAAAAGAGAGAGAGCAGCAGCAACGTGAAATCC 545

Qy   589 TGCATGAGATTCAGAGAGGAAAGAGATAAAAGAGAAGAGAAAAAAGGAAAGAAAGAAATGG 648
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 TGCATGAGATTCAGAGAGGAAAGAGATAAAAGAGAAGAGAAAAAAGGAAAGAAAGAAATGG 605

Qy   649 CTAAGCAGGAAACGTTTGGAAATTGCTACGTTTGTCAAACCAAGATCATCACCTCTAAGAAGG 708
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 CTAAGCAGGAAACGTTTGGAAATTGCTACGTTTGTCAAACCAAGATCATCACCTCTAAGAAGG 665

Qy   709 ACCCAGGAGGACACAGAACGGCTGCCATTCTACCATGGAGGCTCTCCTGACTTTGTGTAGGAA 768
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 ACCCAGGAGGACACAGAACGGCTGCCATTCTCACCATGGAGGCTCTCCTGACTTTGTGTAGGAA 725

Qy   769 ATGGTAAACATCGGGCAAACTCCTCAGGAAGGTCTAGGCGAAGCGTCAGTATTCTGTAT 828
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726 ATGGTAAACATCGGGCAAACTCCTCAGGAAGGTCTAGGCGAAGCGTCAGTATTCTGTAT 785

Qy   829 GTAATAGTGAAGATTCTGTATTCAATATGGGGAGTCCTG 888
            |||||||||||||||||||||||||||||||||||||||
Db   786 GTAATAGTGAAGATTCTGTATTCAATATGGGGAGTCCTG 845

Qy   889 ATCAGCTCATGGTGCACAAAGGGAAATGTATTGCAGTGATGAACAACTTGAAAATTAG 948
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   846 ATCAGCTCATGGTGCACAAAGGGAAATGTATTGCAGTGATGAACAACTTGAAAATTAG 905

Qy   949 TCTACAATGCTTTGGAAACAGCCACTGGCTTTGTCTTGTTGTATGAGTGGGTCCTTC 1008
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   906 TCTACAATGCTTTGGAAACAGCCACTGGCTTTGTCTTGTTGTATGAGTGGGTCCTTC 965

Qy   1009 AGTGGCAGAAAAAATGGTCCATTCCTTACCAGTCAAGAAAAGAGATTGATAAGT 1068
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   966 AGTGGCAGAAAAAATGGTCCATTCCTTACCAGTCAAGAAAAGAGATTGATAAGT 1025

Qy   1069 GCAAAAAGCAGATTCAAGAACAGAAACAGAATCAACTCACTGGTAAAATTGAGCCATC 1128
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 GCAAAAAGCAGATTCAAGAACAGAAACAGAATCAACTCACTGGTAAAATTGAGCCATC 1085

Qy   1129 CAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGACGCAAGACGACTCCATCGTGGTGG 1188
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086 CAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGACGCAAGACGACTCCATCGTGGTGG 1145

Qy   1189 ACATTTTAGTGGAGCACATTAGTGGGGTCTCTTGCTGCACACCTGCACACTCAGCC 1248

Right column (Db / Qy alignment, positions 2226–3408 / 2285–3365):

```
Db  2226 ACGACGAGGACGACGCACGGTGGCGTCTTCTCCCAGTCGTTCTTCTGCGCTGCTTCAGATTCTG 2285
Qy  2329 AAAGTGATATTATCTTTGACAATGAGAGATGAGAACAAGTAAAAGTCAGAATCAGGATGAAG 2388
Db  2286 AAAGTGATATTATTCTTTGACAATGAGAGATGAGAACAGTAAAAGTCAGAATCAGGATGAAG 2345
Qy  2389 ATTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGCTGTGC 2448
Db  2346 ATTGCAATGAAAAGAAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGCTGTGC 2405
Qy  2449 ACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTACGAGACCACCATTGACC 2508
Db  2406 ACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTACGAGACACCATTGACC 2465
Qy  2509 AGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTCGAGAGATTCTGTCAACATTGGAT 2568
Db  2466 AGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTCGAGAGATTCTGTCAACATTGGAT 2525
Qy  2569 TAGCTTATATCCATGAAAGGAATGATTCACCGGGATTTGAAGCCTGTGTCAACATTTTT 2628
Db  2526 TAGCTTATATCCATGAAAGGAATGATTCACCGGGATTTGAAGCCTGTGTCAACATTTTT 2585
Qy  2629 TGGATTCTGATGACCATGTGAAAATAGGTGATTTTGGTTGGCGACAGACCATCTAGCCT 2688
Db  2586 TGGATTCTGATGACCATGTGAAAATAGGTGATTTTGGTTGGCGACAGACCATCTAGCCT 2645
Qy  2689 TTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCCTTCAG 2748
Db  2646 TTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCCTTCAG 2705
Qy  2749 GTCACTTAACTGGGATGGTTGGCACTGCTCTCTATGTGAAGCCCAGGAGGTCCAAGGAGGCA 2808
Db  2706 GTCACTTAACTGGGATGGTTGGCACTGCTCTCTATGTGAAGCCCAGGAGGTCCAAGGAGGCA 2765
Qy  2809 CCAAATCTGCATACAACCAGAAAGTGGATCTTCAGCCTGGGAATTATCTTCTTTGAGA 2868
Db  2766 CCAAATCTGCATACAACCAGAAAGTGGATCTTCAGCCTGGGAATTATCTTCTTTGAGA 2825
Qy  2869 TGTCCTATCACCCCATGTCACGGCTTGTTCTCAACCAACTCAGAG 2928
Db  2826 TGTCCTATCACCCCATGTCACGGCTTGTTCTCCACCAACTCAGAG 2885
Qy  2929 ATCCCACTTCGCCTAAGTTCGACGATGGAGCATGCAAAGCAGAAAT 2988
Db  2886 ATCCCACTTCGCCTAAGTTCGACGATGGAGCATGCAAAGCAGAAAT 2945
Qy  2989 CAGTCATCCTGGCTGTGAACCACGATCCAGCAAAACGGCCCACAGCCAGAACTGC 3048
Db  2946 CAGTCATCCTGGCTGTGAACCACGATCCAGCAAAACGGCCCACAGCCAGAACTGC 3005
Qy  3049 TCAAGAGTGAGCTGCTGCCCCCACCCCCACCCCCACCCAGATGGAAGGCCATGCAAGTGCTGC 3108
Db  3006 TCAAGAGTGAGCTGCTGCCCCCACCCCCACCCCCACCCAGATGGAAGGCCATGCAAGTGCTGC 3065
Qy  3109 ACCACACGCTGACCACGTGGATGGGAAGGCCTACCGCACATGACGATCTTCT 3168
Db  3066 ACCACACGCTGACCACGTGGATGGGAAGGCCTACCGCACATGACGATCTTCT 3125
Qy  3169 CGCAGCGCATCTCCCCTGCCATCGATTACCTATGACAGCGACATACTGAAGGGCAACT 3228
Db  3126 CGCAGCGCATCTCCCCTGCCATCGATTACCTATGACAGCGACATACTGAAGGGCAACT 3185
Qy  3229 TCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGCATCTTTA 3288
Db  3186 TCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGCATCTTTA 3245
Qy  3289 AAAGACATGGAGCTGTTCAGTTGTGTACTCCACTACTGCTTCCCGAAACAGACAAATAT 3348
Db  3246 AAAGACATGGAGCTGTTCAGTTGTGTACTCCACTACTGCTTCCCGAAACAGACAAATAT 3305
Qy  3349 ATGAGCACAACGAAGCTGCCCTATTCATGGACCACAGCGGGGATGCTGGTGATGCTTCCTT 3408
Db  3306 ATGAGCACAACGAAGCTGCCCTATTCATGGACCACAGCGGGGATGCTGGTGATGCTTCCTT 3365
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Left column (Db / Qy alignment, positions 1146–2328 / 1205–2328):

```
Db  1146 ACATTTTAGTGAGCACATTAGTGGGTCTCTTGCTGCTCACACTTGGAGCCACTCAGGCC 1205
Qy  1249 CCATCCCCTGTGCATCAGCTTCGGCAGTACACAACCCGAGTTCGTTGCTCCTGTCAGGCCTTGATTATC 1308
Db  1206 CCATCCCCTGTGCATCAGCTTCGGCAGTACACAACCCGAGTTCGTTGCTCCTGTCAGGCCTTGATTATC 1265
Qy  1309 TGCACAGCAATTCTGTGGTGCAATAAGGTCCTGAGTGCATCTAATGTCTTGGTGGATGCAG 1368
Db  1266 TGCACAGCAATTCTGTGGTGCAATAAGGTCCTGAGTGCATCTAATGTCTTGGTGGATGCAG 1325
Qy  1369 AAGGCACCGTCAAGATTACGGACTATAGCATTCTAAGCGGCTCGGCAGACATTTGCAAGG 1428
Db  1326 AAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGGCTCGGCAGACATTTGCAAGG 1385
Qy  1429 AGGATGTGTTTGAGCAAACCCGAGTTCGTTGTTTAGTGACAAATGCTCTGCCTTATAAAACGG 1488
Db  1386 AGGATGTGTTTGAGCAAACCCGAGTTCGTTGTTTAGTGACAAATGCTCTGCCTTATAAAACGG 1445
Qy  1489 GGAAGAAAGGAGAGATGTTTGGCGTCTTGGCCTTCGTGTGTCCCAAGCAAGGACAGCAGG 1548
Db  1446 GGAAGAAAGGAGAGATGTTTGGCGTCTTGGCCTTCGTGTGTCCCAAGCAAGGACAGCAGG 1505
Qy  1549 AATGTGGAGAGTACCCTGTGACCATCCTAGTGACTTACCAGCTGACTTTCAAGATTTTC 1608
Db  1506 AATGTGGAGAGTACCCTGTGACCATCCTAGTGACTTACCAGCTGACTTTCAAGATTTTC 1565
Qy  1609 TAAAGAAATGTGTGGGCTTGGATGACAAGGAAAGATGGAGTCCCAGTGTTGTTGAAAC 1668
Db  1566 TAAAGAAATGTGTGGGCTTGGATGACAAGGAAAGATGGAGTCCCAGTGTTGTTGAAAC 1625
Qy  1669 ACAGCTTTATAAATCCCCAGCCAAAAATGCCTCTAGTGGAACAAAGTCCTGAAGATTCTG 1728
Db  1626 ACAGCTTTATAAATCCCCAGCCAAAAATGCCTCTAGTGGAACAAAGTCCTGAAGATTCTG 1685
Qy  1729 GAGGACAAGATTATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCGTGCTGCCTTCT 1788
Db  1686 GAGGACAAGATTATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCGTGCTGCCTTCT 1745
Qy  1789 TTAGTGAGACACAGAGACAGTTTCCCGATACTTCATTGAGTTGAAGAATTACAACTTC 1848
Db  1746 TTAGTGAGACACAGAGACAGTTTCCCGATACTTCATTGAGTTGAAGAATTACAACTTC 1805
Qy  1849 TTGGTAAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTGCTGCT 1908
Db  1806 TTGGTAAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTGCTGCT 1865
Qy  1909 ACGCAGTGAAGCGCATCCCATCAACCCGGCCAGCCGGCGAGCGCAGCAGAACGGCCTTGGACGGGCG 1968
Db  1866 ACGCAGTGAAGCGCATCCCATCAACCCGGCCAGCCGGCGAGCGCAGCAGACGGGCG 1925
Qy  1969 AAGTGACACTGCTGTCACGGCTCGTGTCACGCCTAGTTGTGCGCTACTACAACGCCTGGA 2028
Db  1926 AAGTGACACTGCTGTCACGGCTCGTGTCACGCCTAGTTGTGCGCTACTACAACGCCTGGA 1985
Qy  2029 TCGAGCGGCACCGACCGAGGCGGCCGCCGTTCCCCGCCACCCGGGACTCCGGGCCCCTGG 2088
Db  1986 TCGAGCGGCACCGACCGAGGCGGCCGCCGTTCCCCGCCACCCGGGACTCCGGGCCCCTGG 2045
Qy  2089 CCAAGGATGAACGGCGCATCCCATCAACCCGGCCAGCCGGCGAGCGGACACAGAGCGCTTGGAGGCG 2148
Db  2046 CCAAGGATGAACGGCGCATCCCATCAACCCGGCCAGCCGGCGAGCCGCGACACAGAGCGCTTGGAGGCG 2105
Qy  2149 TAGAGGCGCCGCGCCGCGCCCGCGCCAGCTCGGTGAGTGGAGCGCACTTCGGGCG 2208
Db  2106 TAGAGGCGCCGCGCCGCGCCCGCGCCAGCTCGGTGAGTGGAGCGCACTTCGGGCG 2165
Qy  2209 TCGAGCGGCCGCCGACCGAGCGGGCACGGGCCCGTTCCCCGCCGACTCCGGGCCCCTGG 2268
Db  2166 TCGAGCGGCCGCCGACCGAGCGGGCACGGGCCCGTTTCCCCGCCGACTCCGGGCCCCTGG 2225
Qy  2269 ACGACGAGGACGACGCACGGTGGCGTCTTCTCCCAGTCGTTCTTCTGCGCTGCTTCAGATTCTG 2328
Db  ...
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```
Qy  3409 TTGACCTGCGGATCCCTTTTGCAAGATATGTGCAAGAAATAATATATTGAATTTAAAAC 3468
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Db  3366 TTGACCTGCGGATCCCTTTTGCAAGATATGTGCAAGAAATAATATATTGAATTTAAAAC 3425

Qy  3469 GATACTGCATAGAACGTGTGTTCAGGCCCGCCAAGTTAGATCGATTTCATCCCAAAGAAC 3528
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3426 GATACTGCATAGAACGTGTGTTCAGGCCGCCGCCAAGTTAGATCGATTTCATCCCAAAGAAC 3485

Qy  3529 TTCTGGAGTGTGCATTTGATATTGCACTTCACCACCAACAGCTTTCTGCCCACTGCTG 3588
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3486 TTCTGGAGTGTGCATTTGATATTGCACTTCTCCACCAACAGCTTTCTGCCCACTGCTG 3545

Qy  3589 AAATTATCTACACTATCTATGAAATCATCCAAGAGTTCCAGCACTTCAGGAAAGAAATT 3648
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3546 AAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAGAAATT 3605

Qy  3649 ACAGTATTTATTTGAACCATACCATGTTATTGAAAGCAATACTCCTTACACTGTGGATCC 3708
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3606 ACAGTATTTATTTGAACCATACCATGTTATTGAAAGCAATACTCCTTACACTGTGGGATCC 3665

Qy  3709 CAGAAGATAAACTCAGTCAGTGGAAGCTCACAATATTCTGTATGATGCTGTGACAGAGAAGCTGTC 3768
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3666 CAGAAGATAAACTCAGTCAGTGGAAGCTCACAATATTCTGTATGATGCTGTGACAGAGAAGCTGA 3725

Qy  3769 CGAGGAGAAGTGGAAGCTAAAATTTGTAATCGTGTTTTGTCTTCTTAATAGTCTGTGTC 3828
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3726 CGAGGAGAAGTGGAAGCTAAAATTTGTAATCGTGTTCTTTGTCTTCTTAATAGTCTGTGTC 3785

Qy  3829 GACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAATAAATT 3888
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3786 GACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAATAAATT 3845

Qy  3889 CATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGACCTGA 3948
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3846 CATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGACCTAG 3905

Qy  3949 AGGAGGTTGTTGGACTGTTGGAAGAAACTCGGCATCAAGTTACAGGTCTTGATCAATTGG 4008
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3906 AGGAGGTTGTTGGACTGTTGGAAGAAACTCGGCATCAAGTTACAGGTCTTGATCAATTGG 3965

Qy  4009 GCTTGGTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTTCATCA 4068
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3966 GCTTGGTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTTCATCA 4025

Qy  4069 AACGAAGGCAAAGGGCGTGTACCTGGAAATCCTCGCAGCTGGAGGCAGATATGACCTGCTGA 4128
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4026 AACGAAGGCAAAGGGCGTGTACCTGGAAATCCTCGCAGCTGGAGGCAGATATGACCTGCTGA 4085

Qy  4129 TTTCCCAGTTTAGAGGGGCCACAAGCTCTTGGGGCCAGTTCCCACTGGGGTCAGCA 4188
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4086 TTTCCCAGTTTAGAGGGGCCACAAGCTCTTGGGGCCAGTTCCCACTGGGGTCAGCA 4145

Qy  4189 TAGCTATAGACAAGATATCTGCTGCTGTCCTCAACATGGAGAATCTCTTACAATAAGCT 4248
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4146 TAGCTATAGACAAGATATCTGCTGCTGTCCTCAACATGGAGAATCTCTTACAATAAGCT 4205

Qy  4249 CTTGTTGACCTCCTGGTTGTAAGTGTTGGTGTCAGATGTCTATGTCCAGGGCCATCAACCTAA 4308
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4206 CTTGTTGACCTCCTGGTTGTAAGTGTTGGTGTCAGATGTCTATGTCCAGGGCCATCAACCTAA 4265

Qy  4309 CCCAGAAACTTGGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACAGTCCC 4368
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4266 CCCAGAAACTTGGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACAGTCCC 4325

Qy  4369 AAGAGGAATTACAAGAGTACTGCAGACATCTGCAGATCATGAAATCACCTATGTGGCCCTTGTCTCGG 4428
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4326 AAGAGGAATTACAAGAGTACTGCAGACATCTGCAGACATCACCTATGTGCCCTTGTCTCGG 4385

Qy  4429 ATAAAGAGGAAGCCATGTCAAGGTTAAGTCTTTCGAGAAGAAAGCAGACAGAGAAGC 4488
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4386 ATAAAGAGGAAGCCATGTCAAGGTTAAGTCTTTCGAGAAGAAAGCAGACAGAGAAGC 4445
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Qy  4489 GTGTGCTGGAGACTGAACTTGTGGACCATGTGTGGACCATGTGGACCTACTGCGAGAAACTGAGGACTAAAGTCACTG 4548
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4446 GTGTGCTGGAGACTGAACTTGTGGACCATGTGGACCATGTGGACCTACTGCGAGAAACTGAGGACTAAAGTCACTG 4505

Qy  4549 ATGAAAGGAATGGCAGAGAGAGCTTCCGATAATCTTCGAGTGCAAAATCTGAAGGGGTCAT 4608
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4506 ATGAAAGGAATGGCAGAGAGAGCTTCCGATAATCTTCGAGTGCAAAATCTGAAGGGGTCAT 4565

Qy  4609 TTTCTAATGCTTCAGGTTGTTGAAATCCATGGAGCAACAGTGGTTCCCATTGTGAGTG 4668
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4566 TTTCTAATGCTTCAGGTTGTTGAATTCCATGGAGCAACAGTGGTTCCCATTGTGAGTG 4625

Qy  4669 TGCTAGCCCGGAAGCTGTCGCAGCCACACTAGGAGGCGGCGCTATGAAAACTCAGGTACAAA 4728
         ||||||||||||||||||||||||||||||||||||||||||||||          |
Db  4626 TGCTAGCCCGGAAGCTGTCGCAGCCACACTAGGAGGCGGCGCTATGAAAACTCTG------ 4678

Qy  4729 CTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAGCAGTGAAATTGAAATTCTGG 4788
         
Db  4679 ------------------------------------------------------------ 4679

Qy  4789 CTGTGGATCTACCCAAAGAAACAATATTACAGTTTTATCATTAGAGTGGGATGCTGATG 4848
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4679 --GTGGATCTACCCAAAGAAACAATATTACAGTTTTATCATTAGAGTGGGATGCTGATG 4736

Qy  4849 AACAGGCATTAACACAACTGTGAAGCAGCTGCTGTCACGCGCCTGCCAAAGCAAAGATACC 4908
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4737 AACAGGCATTTAACAACAACTGTGAAGCAGCTGCTGTCACGCGCCTGCCAAAGCAAAGATACC 4796

Qy  4909 TCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAGGTGTCTGTGTCTAT 4968
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4797 TCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAAGTGTCTGTGTCTAT 4856

Qy  4969 TTTCTGTACAGCTATAGAGATGACTACTACAGAATCCTATTTTAACCCTAAAGAACTGTCG 5028
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4857 TTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAACCCTAAAGAACTGTG 4916

Qy  5029 TTAACCTCATTCAAACACGACAGAGGCTTATACTGGAATAATGAATGTTGTACATTCATC 5088
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Db  4917 TTAACCTCATTCAAACACGACAGAGGCTTATACTGGAATAATGAATGTTGTACATTCATC 4976

Qy  5089 ATAATTAAAATTAAAATTCTAAGAAGAGGCTGGTCAGTGGTCTCACACCTTTAATCCCA 5148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4977 ATAATTAAAATTAAAATTCTAAGAAGAGGCTGGTCAGTGGTCTCACACCTTTAATCCCA 5036

Qy  5149 GCACTTTGGGAAGCCAAGGCAGGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCCT 5206
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Db  5037 GCACTTTGGGAAGCCAAGGCAGGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCCT 5094
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RESULT 5
US-09-842-758-3
; Sequence 3, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shimkets, Richard A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tcherney, Velizar T
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E
; APPLICANT: Gangolli, Esha A
; APPLICANT: Smithson, Glennda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier, Raymond J
; APPLICANT: Grosse, William M

```
;    APPLICANT:  Edward, Szekeres S
;    APPLICANT:  Alsobrook II, John P
;    TITLE OF INVENTION: No. US20030083244A1e1 Proteins and Nucleic Acids Encoding Same
;    FILE REFERENCE: 15966-783
;    CURRENT APPLICATION NUMBER: US/09/842,758
;    CURRENT FILING DATE:  2001-04-25
;    PRIOR APPLICATION NUMBER: 60/200,158
;    PRIOR FILING DATE:  2000-04-26
;    PRIOR APPLICATION NUMBER: 60/200,613
;    PRIOR FILING DATE:  2000-04-28
;    PRIOR APPLICATION NUMBER: 60/200,780
;    PRIOR FILING DATE:  2000-04-28
;    PRIOR APPLICATION NUMBER: 60/201,006
;    PRIOR FILING DATE:  2000-05-01
;    PRIOR APPLICATION NUMBER: 60/201,007
;    PRIOR FILING DATE:  2000-05-01
;    PRIOR APPLICATION NUMBER: 60/201,236
;    PRIOR FILING DATE:  2000-05-01
;    PRIOR APPLICATION NUMBER: 60/201,238
;    PRIOR FILING DATE:  2000-05-03
;    PRIOR APPLICATION NUMBER: 60/201,186
;    PRIOR FILING DATE:  2000-05-02
;    PRIOR APPLICATION NUMBER: 60/201,474
;    PRIOR FILING DATE:  2000-05-03
;    PRIOR APPLICATION NUMBER: 60/201,508
;    PRIOR FILING DATE:  2000-05-03
;    PRIOR APPLICATION NUMBER: 60/220,591
;    PRIOR FILING DATE:  2000-07-25
;    PRIOR APPLICATION NUMBER: 60/232,678
;    PRIOR FILING DATE:  2000-09-15
;    PRIOR APPLICATION NUMBER: 60/263,217
;    PRIOR FILING DATE:  2001-01-22
;    PRIOR APPLICATION NUMBER: 60/265,160
;    PRIOR FILING DATE:  2001-01-30
;    NUMBER OF SEQ ID NOS: 113
;    SOFTWARE: PatentIn Ver. 2.1
US-09-842-758-3
;    SEQ ID NO 3
;    LENGTH: 4989
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-842-758-3

Query Match             85.7%;  Score 4733;  DB 10;  Length 4989;
Best Local Similarity   98.4%;  Pred. No. 0;
Matches 4911;  Conservative    0;  Mismatches   35;  Indels   47;  Gaps   11;

Qy         63 ATGGCTGGGGGCCGTGGGGCGCCCCCGGGCGCGGGCGCGGGCCGCCTCCGGAGCTTCCGGAGCGAGAGCTACCCG 122
              ||||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTGGGGGCCGTGGGGCGCCCCCGGGCGCGGGCGCGGGCCGCCTCCGGAGCTTCCGGAGCGAGAGCTACCCG 60

Qy        123 CAACGACAGAGACCACGAGCTACAGGCCCTGGAGGCCATCTACGGCGCGACTTCCAAGAC 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAACGACAGAGACCACGAGCTACAGGCCCTGGAGGCCATCTACGGCGCGACTTCCAAGAC 120

Qy        183 CTGCGGCGGCGGACGCTTGCGGACC-----GGTCAAAGAGCCCCTGAAATCAATTTAGTT 236
              ||||||||||||||||||||||||      |||||||||||||||||||||||||||||| 
Db        121 CTGCGGCGGCGGACGCTTGCGGACCCGGTTAAGGTCAAAGAGCCCCTGAAATCAATTTAGTT 180

Qy        237 TTGTACCCTCAAGGCCTAACTGGTGAAGAGTAGTCCTGAAATAGAGTTAAAAAATGCCAAGGTCTA 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTGTACCCTCAAGGCCTAACTGGTGAAGAGTAGTCCTGAAATAGAGTTAAAAAATGCCAAGGTTAAA 240

Qy        297 TGCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAATGCCAAGGTCTA 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAATGCCAAGGTCTA 300

Qy        357 TCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAAGAACTGGCCAAGAAACACTGT 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAAGAACTGGCCAAGAAACACTGT 360

Qy        417 GGGGAG---GTGATGGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCTCAGCGAGCAT 473
              |||||     |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGGGAGGTAGTGATGGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCTCAGCGAGCAT 420
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Qy        474 AACAAGCCCCTCCCCAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGCTCAGGAGGAG 533
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAAGCCCCTCCCCAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGCTCAGGAGGAG 480

Qy        534 CAGCAGAGGCTGTTGGAGGCCAAGCGAGCAGGAGAGCAGGAGCAACGTGAAATCCTGCAT 593
              ||||||||||||||| |  ||||||||||||||||||||||||||||||||||||||||||
Db        481 CAACAGAGGCTGTTGGAGGCCCAAGCGGAAGAGAGAGAGCACAGCAACGTGAAATCCTGCAT 540

Qy        594 GAGATTCAGAGAGGAAAGGAAAGGAAGAAGATAAAGAGAAGAGGAAAAAAGGAAAGAAATGGCTAAG 653
              ||||||| ||||||||||||||||||||     |||||||||||     |||||||||||||||||||
Db        541 GAGATTCAGAGAAGGAAAGGAAGAAGATAAAGAGAAGAGGAAAAAAGAAAAGAAATGGCTAAG 600

Qy        654 CAGGAACGTTGGAAAATTGCTAGTTGTCAAACCAAGATCATACCCTCAAGAAGGACCCA 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGAACGTTGGAAAATTGCTAGTTGTTGTCAAACCAAGATCATACCTCTCAAGAAGGACCCA 660

Qy        714 GGAGGACACAGAACGGCTCCATTCACATGGAGGCTCCTCCGACTTTGTAGGGAAATGGT 773
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGAGGACACAGAACGGCTCCATTCTACATGGAGGCTCCTCCTGACTTTGTAGGGAAATGGT 720

Qy        774 AAACATCGGGCAAACTCCTCAGGAAGGTCT------AGGCGAGAACGTCAGTATTCTGTA 827
              ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||
Db        721 AAACATCGGGCAAACTCCTCAGGAAGGTCTAGGTTAAGGCGAGAACGTCAGTATTCTGTA 780

Qy        828 TGTAATAGTGAAGATTCTCCTGGCTCTTGTGAATTCTGTATTCAATATGGGAGTCCT 887
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGTAATAGTGAAGATTCTCCTGGCTCTTGTGAATTCTGTATTCAATATGGGAGTCCT 840

Qy        888 GATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGAACAACTTGAAAATTA 947
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGAACAACTTGAAAAATTA 900

Qy        948 GTCTACCAATGCTTTGGAAACAGCCACTGGTCCATTCCTTACCAGTCAAGAAAAAGAGAAGATTGATAAG 1007
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTCTACCAATGCTTTGGAAACAGCCACTGGTCCATTCCTTGTCCTTGTTGTGATGAGTGGTGGGTCCTT 960

Qy       1008 CAGTGCGAGAAAGCAGATTCAAGGAACAGAACAGAATTCAACTCACTCGGTAAAATTGAGCCAT 1067
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAGTGCGAGAAAGCAGATTCAAGGAACAGAACAGAATTCAACTCACTCGGTAAAATTGAGCCAT 1020

Qy       1068 TGCAAAAAGCAGATTCAAGGAACAGAACAGAATTCAAGGAACAGAACAGACTCCA-TCGTGGT 1127
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1021 TGCAAAAAGCAGATTCAAGGAACAGAACAGAATTCAAGGAACAGAACAGAATGAAT-TCAAAGAGCAAGAGCAAGACGACTCCATTCATTCGTGGT 1080

Qy       1128 CCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGAGCAAGACGACTCCA-TCGTGGT 1186
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGAGCAAGACGACTCCATTCATTCGTGTGT 1139

Qy       1187 GGACATTTTAGTGGAGCACATTAGTGGGTTCTCTTGCTGCTACACCTGAGCCACTCAGG 1246
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1140 GGACATTTTAGTGGAGCACATTAGTGGGTTCTCTTGCTGCACCTGAGCCACTCAGG 1199

Qy       1247 CCCCATCCCTGTGCATCAGCTTGGCAGGTACACAGCTCAGCTCCTGTCAGGCCTTGATTA 1306
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 CCCCATCCCTGTGCATCAGCTTGGCAGGTACACAGCTCAGCTCCTGTCAGGCCTTGATTA 1259

Qy       1307 TCTGCACAGCAATTCTGTGGTGCAATAGCATTCTAAGCGCCTATAGCATTTGCAA 1366
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1260 TCTGCACAGCAATTCTGTGGTGCAATAGCATTCTAAGCGCCTATAGCACATTTGCAA 1319

Qy       1367 AGAAGGCACCGTCAAGATTACGGACTATAGCATTCTAAGCGCCTCGAACAATTTGCAA 1426
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 AGAAGGCACCGTCAAGATTACGGACTATAGCATTCTAAGCGCCTCGAACACATTTGCAA 1379

Qy       1427 GGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTAGTGACAATGCTCTGCCTTATAAAAC 1486
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1380 GGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTAGTGACAATGCTCTGCCTTATAAAAC 1439

Qy       1487 GGGGAAGAAGTGTTTGGCGTCTTGGCCTTCGTCCGTCCCTCAGCCAAGGACA 1546
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1440 GGGGAAGAAGGAGATGTTTGGCGTCTTGGCCTTCGTCCGTCCCTCAGCCAAGGACA 1499
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Qy   1547 GGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGATTT 1606
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Db   1500 GGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGATTT 1559

Qy   1607 TCTAAAGA---ATGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTT 1663
          |||||||    |||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 TCTAAAGAGAGACAGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTT 1619

Qy   1664 GAAACACAGCTTTATAAATCCCAGCCAAAAATGCCTCTAGTGACAAGTCCTGAAGA 1723
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 GAAACACAGCTTTATAAATCCCAGCCAAAAATGCCTCTAGTGACAAGTCCTGAA-- 1677

Qy   1724 TTCTGGAGACAAGATATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGC 1783
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1678 -TCTGAAGGACAAGATATTGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGC 1736

Qy   1784 CTTCTTTAGTGAGACACAGACAGCAGTTTCCCGATACTTCATTGAGTTGAAGAATTACA 1843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1737 CTTCTTTAGTGAGACACAGACAGCAGTTTCCCGATACTTCATTGAGTTGAAGAATTACA 1796

Qy   1844 ACTTCTTGGTAAAGGAGAGCTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTG 1903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1797 ACTTCTTGGTAAAGGAGAGCTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTG 1856

Qy   1904 CTGCTACGCAGTGAAGCCGATCCCCATCAACCCGGCCAGTTCCCGGATCAA 1963
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1857 CTGCTACGCAGTGAAGCCGCATCCCCATCAACCCGGCCAGTTCCCGGATCAA 1916

Qy   1964 GGGCCGAAGTGACACTGCTGTCACGGCTGACCATGAGAACATTGTGCGCTACTACAACGC 2023
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1917 GGGCCGAAGTGACACTGCTGTCACGGCTGACCATGAGAACATTGTGCGCTACTACAACGC 1976

Qy   2024 CTGGATCGAGCGGCACAGAGCGCCGGGGACCGGGCGAGGCGCCGGCGACACAGACGCCGGCC 2083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1977 CTGGATCGAGCGGCACAGAGCGCCGGGGACCGGGCGAGGCGCCGGCGACACAGACTCCGGCC 2036

Qy   2084 CCTGGCCAAGGACGATGACCGAGCTGCACGGCGCACGCGGCGACACAGACGCGGCCTGGA 2143
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Db   2037 CCTGGCCAAGGACGATGACCGAGCTGCACGGCGCACGCGGCGACACAGACGCGGCCTGGA 2096

Qy   2144 CAGCGCTAGAGGCCGCGCGCCGCCGCCATCCTCAGCGACTCGGTGAGTGGAGCACTTC 2203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2097 CAGCGCTAGAGGCCGCGCGCCGCCGCCATCCTCAGCGACTCGGTGAGTGGAGCACTTC 2156

Qy   2204 GGGCGAGCGCGTCGGCCAGTGCCCGTTCCCGGCCACCGCCGTTCCCGGGACTCCCAGCATGACGACGA 2263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2157 GGGCGAGCGCGTCGGCCAGTGCCCGTTCCCGGCCACCGCCGTTCCCGGGACTCCCAGCATGACGACGA 2216

Qy   2264 GGACGACGAGGACGAGCAGAGCAGAGCACGCGGCCGCGCGCCGCGAGGCGAGTGACGACTCAGGA 2323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2217 GGACGACGAGGACGAGCAGAGCAGAGCACGCGGCCGCGCGCCGCGAGGCGAGTGACGACTCAGGA 2276

Qy   2324 TTCTGAAAGTGCAATGCAATGAAAAGAATGGCTGCCATGGCCATGAGAACAGTAAAGTCAGATCAGGA 2383
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2277 TTCTGAAAGTGCAATGATATATCTTTGACAATGGCTGCCATGGCCATGAGAACAGTAAAGTCAGATCAGGA 2336

Qy   2384 TGAAGATTGCAATGAAAAGAATGGCTGCCATGAGAGCGTCAGTGCCATCCATGAAAGTGAGACTGAGGC 2443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2337 TGAAGATTGCAATGAAAAGAATGGCTGCCATGAGAGCGTCAGTGCCATCCATGAAAGTGAGACTGAGGC 2396

Qy   2444 TGTGCACTACCTATCGTATCGAGACACCGTGAGCTCTGGAGGCTTTTTTGAGAGATTCTGGA 2503
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Db   2397 TGTGCACTACCTATCGTATCGAGACACCGTGAGCTCTGGAGGCTTTTTTGAGAGATTCTGGA 2456

Qy   2504 TGACCAGGGGACTCGTATCCGAGACTCGGAGACTCGGAGGCCTTTTTCACCGGGATTGGTCAACAT 2563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2457 TGACCAGGGGACTCGTATCCGAGACTCGGAGACTCGGAGGCCTTTTTCACCGGGATTGGTCAACAT 2516

Qy   2564 TGGATTAGCTTATATCCATGAGGAAAGGAATGATTCACCCGGGATTTGAAGCCTGTCAACAT 2623
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2517 TGGATTAGCTTATATCCATGAGGAAAGGAATGATTCACCCGGGATTTGAAGCCTGTCAACAT 2576

Qy   2624 TTTTTTTGGATTCTGATGACCATGTGAAAAATAGGTGATTTTGGTTTGGCGACACAGACCATCT 2683
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2577 TTTTTTTGGATTCTGATGACCATGTGAAAAATAGGTGATTTTGGTTTGGCGACACAGACCATCT 2636

Qy   2684 AGCCTTTTCTGCTGCACAGCAAACAGACGATCAGACAGCAGACTTGATTAAGTAAGTCAGACCC 2743
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2637 AGCCTTTTCTGCTGCACAGCAAACAGACGATCAGACAGCAGACTTGATTAAGTAAGTCAGACCC 2696

Qy   2744 TTCAGGTGCACTTAACTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGG 2803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2697 TTCAGGTGCACTTAACTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGG 2756

Qy   2804 AAGCACCAAATGTCGATACAACAGAAAGTGGATCCTTCCAGCCTGGGAATTATCTTCTT 2863
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2757 AAGCACCAAATGTCGATACAACAGAAAGTGGATCTTCCAGCCTGGGAATTATCTTCTT 2816

Qy   2864 TGAGATGTCCATCATCACCCCCATGTCACGGCGTCACGGGCTTCAGAAGGATCTTGTGTTCTCAACCAACT 2923
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Db   2817 TGAGATGTCCATCATCACCCCCATGTCACGGCGTCACGGGCTTCAGAAGGATCTTGTGTTCTCAACCAACT 2876

Qy   2924 CAGAGATCCCACTTCGCCTAAGTTCCAGAGACTTTGACGATGGAGCAGCATGCAAAGCA 2983
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Db   2877 CAGAGATCCCACTTCGCCTAAGTTCCAGAGACTTTGACGATGGAGCAGCATGCAAAGCA 2936

Qy   2984 GAAATCAGTCATCTCCTGGCTGTGTGAACCACGATCCAGCAGAAACGGCCCACAGCCACAGA 3043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2937 GAAATCAGTCATCTCCTGCGTGTTGAACCACGATCCAGCAGAAACGGCCCACAGCCACAGA 2996

Qy   3044 ACTGCTCAAGAGTGAGCTGCTGCCCCCAGCAACCCCCCACCCGGAGGAGTCAGAGCTGCATGAAGT 3103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2997 ACTGCTCAAGAGTGAGCTGCTGCCCCCAGCAACCCCCACCCGGAGGAGTCAGAGCTGCATGAAGT 3056

Qy   3104 GCTGCCACCACACCTGACCGCTGCGGGAACGGCGCCGCCTACCGGACCATGATGGCCCAGAT 3163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3057 GCTGCCACCACACCTGACCGCTGCGGGAACGGCGCCGCCTACCGGACCATGATGGCCCAGAT 3116

Qy   3164 CTTGGGCTGAGCGCATCTCCCCTGCCATCGATCGATTACACCTTATGACAGCGACATACAGGAGGG 3223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3117 CTTGGGCTGAGCGCATCTCCCCTGCCATCGATCGATTACACCTTATGACAGCGACATACAGGAGGG 3176

Qy   3224 CAGCGCTAGAGGCCTGGAACCGCGGCCGAGACTCTCAGCGACTCGTGTGAAACCATCATCCGGAT 3283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3177 CAGCGCTAGAGGCCTGGAACCGCGGCCGAGACTCTCAGCGACTCGTGTGAAACCATCATCCGGAT 3236

Qy   3284 CTTTAAAAGACATGGCTGGGGATCCTTCCTGCTCGCGACCACCAGCGGGATGTCTGGTGATGCT 3343
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3237 CTTTAAAAGACATGGCTGGGGATCCTTCCTGCTCGCGACCACCAGCGGGATGTCTGGTGATGCT 3296

Qy   3344 AATATATGAGCACAAGAGCTGCCCTATTCATTGGACCACCAGCGGAGAAATATATTGAATTT 3403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3297 AATATATGAGCACAAGAGCTGCCCTATTCATTGGACCACCAGCGGAGAAATATATTGAATTT 3356

Qy   3404 TCCTTTTGACCTGGGCGGGGTGCCTTTTGCAAGATCTTAGGCCGCGCAAGTTAGATCCGATTTCATCCCAA 3463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3357 TCCTTTTGACCTGGGCGGGGTGCCTTTTGCAAGATCTTAGGCCGCGCAAGTTAGATCCGATTTCATCCCAA 3416

Qy   3464 AAAACGGTACTGCATAGAACGTGTTCACGCGCCGCGCACGCTTCACCACCAACATCCCCAA 3523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3417 AAAACGGTACTGCATAGAACGTGTTCACGCGCCGCGCACGCTTCACCACCAACATCCCCAC 3476

Qy   3524 AGAACTTCTGAATATCTCGGAGTGTGCATTGTGATTGTGAAAGCAATACTCTTACTGTGG 3583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3477 AGAACTTCTGAATATCTCGGAGTGTGCATTGTGATTGTGAAAGCAATACTCTTACTGTGG 3536

Qy   3584 AAATTACAGTATTATTTGAACCATACCATGTTATTGAAAAGCAATACTCTTACTGTGTGG 3643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3537 AAATTACAGTATTATTTGAACCATACCATGTTATTGAAAAGCAATACTCTTACTGTGTGG 3596

Qy   3644 GATCCCAGAAGATAAACTCAGTCAGTAAACATTATTCGTGTATGATGTGCTGCAGAGAA 3703
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3597 GATCCCAGAAGATAAACTCAGTCAGTAAACATTATTCGTGTATGATGTGCTGCAGAGAA 3656
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Db  3657 GATCCCAGAAGATAAACTCAGTCTCACATTATTCTGTATGATGCTGTGACAGAGAA 3716
Qy  3764 GCTGACGAGGAGGAAGTGGAAGCTAAATTTGTAATCGTGTCTTCTTCTAATAGTCT 3823
         |||||||||||||| |||||||||||||||||||||||||| ||| ||||||||||
Db  3717 GCTGACGAGGAGGAGAGTGGAAGCTAAATTTGTAATCGTCTTCGTCTTCTAATAGTCT 3776
Qy  3824 GTGTCGACTTCTACAAGTTTATTGAACAGAGGAGATTGCAAGATCTTATGCCACCAAT 3883
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3777 GTGTCGACTTCTACAAGTTTATTGAACAGAGGAGATTGCAAGATCTTATGCCACCAAT 3836
Qy  3884 AAATTCATTAATAAAACAGAAAACAGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGA 3943
         ||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||
Db  3837 AAATTCATTAATAGAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGA 3896
Qy  3944 CCTAGAGGAGTTGTTGGGACTGTTGAAGAAACTCGGCATCAAGTTACA------GGTCTT 3997
         |||||||||||||||||||||||||||||||||||||||||||||||||      ||||||
Db  3897 CCTAGAGGAGTTGTTGGGACTGTTGGAGAAACTCGGCATCAAGTTACAGGTTTGGGTCTT 3956
Qy  3998 GATCAATTTGGGCTTGGTTGTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGT 4057
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3957 GATCAATTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGT 4016
Qy  4058 GGCTTCATCAAACGAAGGCAAAGGCTGTACCTGAAATCCTGCAGCTGGAGGCAGATA 4117
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4017 GGCTATCATCAAACGAAGGCAAAGGCTGTACCTGAAATCCTGCAGCTGGAGGCAGATA 4076
Qy  4118 TGACCTGCTGATTCCCCAGTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCAT 4177
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4077 TGACCTGCTGATTCCCCAGTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCAT 4136
Qy  4178 TGGGGTCAGCATAGCTATAGACAAGATATCTGCTGTGTCCTCAACATGGAGGAA------ 4232
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4137 TGGGGTCAGCAGCATAGACAAGATATCTGCTGTGTCCTCAACATGGAGGAATTCTGT 4196
Qy  4233 ---TCTGTTACAATAAGCTCTTGTGACCTTCCTGTTGTAAGTGTTGGTCAGATGTCTAT 4288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4197 AAGTTCTGTTACAATAGGCTCTGGGGACCTTCCTGTTGTAAGTGTGGGCCAGATGTCTAT 4256
Qy  4289 GTCCAGGGCCATCAACCTAACCCAGAAACTCTGGACACAGCGCATCACAGCAGAAATCAT 4348
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4257 GTCCAGGGCCATCAAACCTAACCCAGAAATCTCTGGACACAGCGCATCACAGCAGAAATCAT 4316
Qy  4349 GTACGACTGGTCA------CAGTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGA 4402
         |||||||||||||      ||||||||||||||||||||||||||||||||||||||||
Db  4317 GTACGACTGGTCACAGTTTCAGTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGA 4376
Qy  4403 AATCACCTATGTGGCCCTTGCTCGTCCGGATAAGAAGAAGAGCCATGTCAAGGTTAAGTCTTT 4462
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4377 AATCACCTATGTGGCCCTTGCTCGTCCGGATAAGAAGAAGAGCCATGTCAAGGTTAAGTCTTT 4436
Qy  4463 CGAGAAGGAAAGGCAGCAGAGAAGCGTGTGCTGGAGACTGAACTGTGGACCATGTACT 4522
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4437 CGAGAAGGAAAGGCAGCAGAGAAGCGTGTGCTGGAGACTGAACTGTGGACCATGTACT 4496
Qy  4523 GCAGAAACTGAGGACTAAAGTCACTGATGAAAGAAATGGCAGAGAAGCTTCCGATAATCT 4582
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4497 GCAGAAACTGAGGACTAAAGTCACTGATGAAAGAAATGGCAGAGAAGCTTCCGATAATCT 4556
Qy  4583 TGCAGTGCAAAATCTGAAGGGGTCATTTCTAATGCTTCAGGTTTGTTGTTGAAATCCATGG 4642
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4557 TGCAGTGCAAAATCTGAAGGGGTCATTTCTAATGCTTCAGGTTTGTTGTTGAAATCCATGG 4616
Qy  4643 AGCAACAGTGGTTCCCATTGTGAGTGTGCTAGCCCCGGAAGCTTGTCAGCCAGCACTAG 4702
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4617 AGCAACAGTGGTTCCCATTGTGAGTGTGCTAGCCCCGGAAGCTTGTCAGCCAGCACTAG 4676
Qy  4703 GAGGGCCGTATGAAAACTCAGTGAAACTCGACTTCAGAGACTCGCAACTTACATCA 4762
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4677 GAGGGCCGTATGAAAACTCAGTGAAACTCGACTTCAGAGACTCGCAACTTACATCA 4736
Qy  4763 GAAAGCAGTGAAATTGAAATTCTGGCT---GTGGATCTCACCCAAAGAAACAATATTACA 4819
         |||||||||||||||||||||||||||   |||||||||||||||||||||||||||||
Db  4737 GAAAGCAGTGAAATTGAAATTCTGGCTGTGGATCTCACCCAAAGAAACAATATTACA 4796
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Qy  4820 GTTTTTATCATTAGAGTGGGATGCTGATGAACAGGCATTAACACAACTGTGAAGCAGCT 4879
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Db  4797 GTTTTTATCATTAGAGTGGGATGCTGATGAACAGGCATTAACACAACTGTGAAGCAGCT 4856
Qy  4880 GCTGTCACGCCTGCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACAT 4939
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4857 GCTGTCACGCCTGCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACAT 4916
Qy  4940 CAAAGTAGAAAAAAAGGTGTCTGCTATTTCTGTACAGCTATAGAGATGACTACTACAG 4999
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4917 CAAAGTAGAAAAAAAGGTGTCTGCTATTTCTGTACAGCTATAGAGATGACTACTACAG 4976
Qy  5000 AATCTTATTTTAA 5012
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Db  4977 AATCTTATTTTAA 4989
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RESULT 6
US-10-174-333-3
; Sequence 3, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grose, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186

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; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 3
; LENGTH: 4989
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4986)
US-10-174-333-3

Query Match        85.7%;  Score 4733;  DB 12;  Length 4989;
Best Local Similarity   98.4%;  Pred. No. 0;
Matches 4911;  Conservative   0;  Mismatches  35;  Indels  47;  Gaps  11;

Qy     63 ATGGCTGGGGGCCGTGGGGCGTGGGGCCCCGGGGCGGCGCCCGGGGCGGCGAGCCTCCGG 122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCTGGGGGCCGTGGGGCGTGGGGCCCCGGGGCGGCGCCCGGGGCGGCGAGCCTCCGG  60

Qy    123 CAACGACAGGACCCACCAGAGCTACAGGCCCGGGAGCCCATCTACCGCGCGGACTTCCAAGAC 182
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAACGACAGGACCCACCAGAGCTACAGGCCCGGGAGCCCATCTACCGCGCGGACTTCCAAGAC 120

Qy    183 CTGCGGCCGGACGGTTGCGGACC------GGTCAAAGAGCCCCTGAAATCAATTTAGTT 236
          |||||||||||||||||||||||      |||||||||||||||||||||||||||||||
Db    121 CTGCGCGCCGGACGCGTTGCGGACCGGTCAAGAGCCCCTGAAATCAATTTTAGTT 180

Qy    237 TTGTACCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGATTTGAGGGTTAAA 296
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTGTACCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGATTTGAGGGTTAAA 240

Qy    297 TGCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAATGCCAAAGGTCTA 356
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAATGCCAAAGGTCTA 300

Qy    357 TCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAAGAACTGGCCAAGAAACACTGT 416
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAAGAACTGGCCAAGAAACACTGT 360

Qy    417 GGGGAG--GTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTCTCAGCGGAGCAT 473
          ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGGGAGGTAGTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTCTCAGCGGAGCAT 420

Qy    474 AACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGTCAGGAGGAG 533
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGTCAGGAGGAG 480

Qy    534 CAGCAGAGGCTGTTGGAGGCCAAGCAGGCGGAAAGAAGAGCAGCAACGTGAAATCCTGCAT 593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAACAGAGGCTGTTGGAGGCCAAGCAGGCGGAAAGAAGAGCAGCAACGTGAAATCCTGCAT 540

Qy    594 GAGATTCAGAGAAGGAAGGAAGAGAGATAAAAGAAGAGAAAAGAAATGGCTAAG 653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAGATTCAGAGAAGGAAGGAAGAGAGATAAAAGAAGAGAAAAGAAATGGCTAAG 600

Qy    654 CAGGAACGTTTGGAAATTGCTAGTTGTCAAACCAAGATCATACCTCTAAGGAGGACCCA 713
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CAGGAACGTTTGGAAATTGCTAGTTGTCAAACCAAGATCATACCTCTAAGGAGGACCCA 660

Qy    714 GGAGGACACAGACGGCTGCCATTCTACACATGGAGGCTCTCCTGACTTTGTAGGAAATGGT 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGAGGACACAGACGGCTGCCATTCTACACATGGAGGCTCTCCTGACTTTGTAGGAAATGGT 720

Qy    774 AAACATCGGGCAAACTCCTCAGGAAGGTCT------AGGCGAGAACGTCAGTATTCTGTA 827
          |||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db    721 AAACATCGGGCAAACTCCTCAGGAAGGTCTAGGCGAGAACGTCAGTATTCTGTA 780

Qy    828 TGTAATAGTGAAGATTCTCCGGCTTCCTGGCTCTTGTGAATTCTGTATTTCAATATGGGAGTCCT 887
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TGTAATAGTGAAGATTCTCCGGCTTCCTGGCTCTTGTGAATTCTGTATTTCAATATGGGAGTCCT 840

Qy    888 GATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACTTGAAAATTA 947
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACTTGAAAATTA 900
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Qy    948 GTCTACAAATGCTTTGGAAACAGCCACTGGTGGCTTGTCTTGTTGTTATGAGTGGGTCCTT 1007
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTCTACAAATGCTTTGGAAACAGCCACTGGTGGCTTGTCTTGTTGTTATGAGTGGGTCCTT  960

Qy   1008 CAGTGGCAGAAAAAATGGTCATTCCTTACCAGTCAAGAAAAAGAGAAGATTGATAAG 1067
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CAGTGGCAGAAAAAATGGTCATTCCTTACCAGTCAAGAAAAAGAGAAGATTGATAAG 1020

Qy   1068 TGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAGCCAT 1127
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAGCCAT 1080

Qy   1128 CCAAATGTAGTACCCTACCTTGCAATGAATCTCAAAGACAAGAGCAAGAGACTCCA-TCGTGGT 1186
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||| ||||||||
Db   1081 CCAAATGTAGTACCCTACCTTGCAATGAAT-TCAAAGAGCAAGAGCAAGAGACTCCATTCGTGGT 1139

Qy   1187 GGACATTTTAGTGAGCACATTAGTGGGTCCTCTCTTGCTGACACCTGAGCCACTCAGG 1246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 GGACATTTTAGTGAGCACATTAGTGGGTCTCTCTTGCTGCACACCTGAGCCACTCAGG 1199

Qy   1247 CCCCATCCCTGTCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTCAGGCCTTGATTA 1306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 CCCCATCCCTGTCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTCAGGCCTTGATTA 1259

Qy   1307 TCTGCACAGCAATTCTGTGGTGCATAAGGTCCTGAGTGCATCTAATGTCTTGGTGGATGC 1366
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 TCTGCACAGCAATTCTGTGGTGCATAAGGTCCTGAGTGCATCTAATGTCTTGGTGGATGC 1319

Qy   1367 AGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGGCCTCCGCAGACATTTGCAA 1426
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 AGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGGCCTCCGCAGACATTTGCAA 1379

Qy   1427 GGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAAATGCTCTGCCTTATAAAAC 1486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 GGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAAATGCTCTGCCTTATAAAAC 1439

Qy   1487 GGGGAAGAAAGGAGAATGTTTGGCCTTCTCGCGTCGTGTCCCCAGCCAAGACA 1546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1440 GGGGAAGAAAGGAGAATGTTTGGCCTTCTCGCGTCGTGTCCCCAGCCAAGACA 1499

Qy   1547 GGAATGTGGAGAGTACCCTGTGACCATCCCAGTGACTTACCAGCTTTCAAGATTT 1606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 GGAATGTGGAGAGTACCCTGTGACCATCCCAGTGACTTACCAGCTTTCAAGATTT 1559

Qy   1607 TCTAAAGAA---ATGTGTGCTTGGATGACAAGGAAGATGAGTCCCAGCAGTTGTT 1663
          |||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db   1560 TCTAAAGAGAGATGTGTGCTTGGATGACAAGGAAGATGAGTCCCAGCAGTTGTT 1619

Qy   1664 GAAACACAGCTTTATAAATCCCCAGCCAAAAAAATGCCTCTAGTGCAACAAAGTCCTGAAGA 1723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 GAAACACAGCTTTATAAATCCCCAGCCAAAAAAATGCCTCTAGTGCAACAAAGTCCTGAA-- 1677

Qy   1724 TTCTGGAGGACAAGATTATGTTGCTTGAGACTGTTATTCCTCAGCAACCGGCTACCCAGTGCTGC 1783
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1678 -TTCTGGAGGACAAGATTATGTTGCTTGAGACTGTTATTCCTCAGCAACCGGCTACCCAGTGCTGC 1736

Qy   1784 CTTCTTAGTGAGACACAGAGACAGTTTTCCGATACTTCATTGAGTTTGAAGAATTACA 1843
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1737 CTTCTTAGTGAGACACAGAGACAGTTTTCCGATACTTCATTGAGTTTGAAGAATTACA 1796

Qy   1844 ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCATCAAGTGCGAGAACAAGTTGACGGCGCTG 1903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1797 ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCATCAAGTGCAGAACAAGTTGGACGGCGCTG 1856

Qy   1904 CTGCTACGGACGTGAAGCCATCCCATCAACCCGGCAGCCCGGCAGTTCCGCAGGATCAA 1963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1857 CTGCTACGGACGTGAAGCCGCATCCCATCAACCCGGCAGTTCCGCAGGATCAA 1916

Qy   1964 GGGCGAAGTGACACTGCTTGTCACGGCTGCACCATTGTGCGCTACTACAACGC 2023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1917 GGGCGAAGTGACACTGCTTGTCACGGCTGCACCATTGTGCGCTACTACAACGC 1976
```

This page contains a DNA sequence alignment (query "Qy" versus database "Db") presented as paired rows of nucleotide sequences with match bars. The alignment is printed rotated on the page and spans the following residue-position ranges:

Right-hand block (positions ~3057–4232):

Label	Start	End
Qy	3057	3116
Db	—	3223
Qy	3117	3176
Db	—	3283
Qy	3224	3283
Db	3177	3236
Qy	3284	3343
Db	3237	3296
Qy	3344	3403
Db	3297	3356
Qy	3404	3463
Db	3357	3416
Qy	3464	3523
Db	3417	3476
Qy	3524	3583
Db	3477	3536
Qy	3584	3643
Db	3537	3596
Qy	3644	3703
Db	3597	3656
Qy	3704	3763
Db	3657	3716
Qy	3764	3823
Db	3717	3776
Qy	3824	3883
Db	3777	3836
Qy	3884	3943
Db	3837	3896
Qy	3944	3997
Db	3897	3956
Qy	3998	4057
Db	3957	4016
Qy	4058	4117
Db	4017	4076
Qy	4118	4177
Db	4077	4136
Qy	4178	4232

Left-hand block (positions ~1977–3163):

Label	Start	End
Qy	2024	2083
Db	1977	2036
Qy	2084	2143
Db	2037	2096
Qy	2144	2203
Db	2097	2156
Qy	2204	2263
Db	2157	2216
Qy	2264	2323
Db	2217	2276
Qy	2324	2383
Db	2277	2336
Qy	2384	2443
Db	2337	2396
Qy	2444	2503
Db	2397	2456
Qy	2504	2563
Db	2457	2516
Qy	2564	2623
Db	2517	2576
Qy	2624	2683
Db	2577	2636
Qy	2684	2743
Db	2637	2696
Qy	2744	2803
Db	2697	2756
Qy	2804	2863
Db	2757	2816
Qy	2864	2923
Db	2817	2876
Qy	2924	2983
Db	2877	2936
Qy	2984	3043
Db	2937	2996
Qy	3044	3103
Db	2997	3056
Qy	3104	3163

APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pt_FL_genes Version 5.0
SEQ ID NO 90
LENGTH: 4861
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (364)..(4497)
US-10-112-944-90

Query Match   80.8%; Score 4462.4; DB 12; Length 4861;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4474; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

[Sequence alignment data]

RESULT 7
US-10-112-944-90
; Sequence 90, Application US/10112944
; Publication No. US20040048249A1
GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika

```
Db    623 TAGTACGCTACCTTGCAATGAATCTCAAAGAGACAAGACGACTCCATCGTGGTGGACATTT  682
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1195 TAGTGGAGCACATTAGTGGGGTCTTCTTGCTGCTGCTGCTCCTGCTGCTGCTCCTGCTGCTCTCCGCACCTGAGCCACTCAGGCCCCATCC 1254

Db    683 TAGTGGAGCACATTAGTGGGGTCTTCTTGCTGCTGCTCTCCGCACCTGAGCCACTCAGGCCCCATCC  742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1255 CTGTGCATCAGCTTCGCAGTACACAGCTCAGCTCCTGTCAGGCCTTGATTATCTGCACA 1314

Db    743 CTGTGCATCAGCTTCGCAGTACACAGCTCAGCTCCTGTCAGGCCTTGATTATCTGCACA  802

Qy   1315 GCAATTCTGTGTGCATAAGGTCCTGAGATGCATCTAATGTCTTGGTGGATGCAGAAGGCA 1374
Db    803 GCAATTCTGTGTGCATAAGGTCCTGAGATGCATCTAATGTCTTGGTGGATGCAGAAGGCA  862

Qy   1375 CCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTGCAAGGAGGATG 1434
Db    863 CCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTGCAAGGAGGATG  922

Qy   1435 TGTTTGAGCAAACCCGAGTTCGTTTAGTGACAATGCTCGTGTCCCTTATAAAACGGGGAAGA 1494
Db    923 TGTTTGAGCAAACCCGAGTTCGTTTAGTGACAATGCTCGTGTCCCTTATAAAACGGGGAAGA  982

Qy   1495 AAGGAGATGTTTGGGCTCTTGGCCTTCTGCGTGCTTGGCCTTCAGCCAAGCAGCAGGAATGTG 1554
Db    983 AAGGAGATGTTTGGGCTCTTGGCCTTCTGCGTGCTTGGCCTTCAGCCAAGCAGCAGGAATGTG 1042

Qy   1555 GAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGAGTCCCAGCAGTTGTTGAAACACAGCT 1614
Db   1043 GAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGAGTCCCAGCAGTTGTTGAAACACAGCT 1102

Qy   1615 AATGTGTGCTTGGATGACAAGAAAAGAGATGGAGTCCCGACAGTTCTGAAGCAAGCAGTTCTGGAAGATTCTGAAGCAAGC 1674
Db   1103 AATGTGTGCTTGGATGACAAGAAAAGAGATGGAGTCCCGACAGTTCTGAAGCAAGCAGTT 1162

Qy   1675 TTATAAATCCCAGCCAAAAATGCCTCTAGTGAACAAAGTGCTACCGGCTACCAGGAGGAC 1734
Db   1163 TTATAAATCCCAGCCAAAAATGCCTCTAGTGAACAAAGTGCTACCGGCTACCAGGAGGAC 1222

Qy   1735 AAGATTATGTTGAGACTGTATTCCTAGCAACCGGCTGCAGACCGGCTGCAGATCAAGAAGTGTCTTAGTG 1794
Db   1223 AAGATTATGTTGAGACTGTATTCCTAGCAACCGGCTGCAGATCAAGAAGTGTCTTAGTG 1282

Qy   1795 AGACACAGAGACAGTTTCCCGATACTTCATTGAGTTGAAGAATTACAACTTCTTGGTA 1854
Db   1283 AGACACAGAGACAGTTTCCCGATACTTCATTGAGTTGAAGAATTACAACTTCTTGGTA 1342

Qy   1855 AAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTGCTGCTACGGAG 1914
Db   1343 AAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTGCTGCTACGGAG 1402

Qy   1915 TGAAGGCCATCCCATCAACCCGGCAGTTCCGCGAGCCCAGGGCCAGTCCCAGGATCAAGGGGCGAAGTGA 1974
Db   1403 TGAAGGCCATCCCATCAACCCGGCAGTTCCGCGAGCCCAGGGCCAGTCCCAGGATCAAGGGGCGAAGTGA 1462

Qy   1975 CACTGCTGTCACGGCTCGCACCGCCACCATGAGACAGTGTGCGCCGCCCCCACCCCAGATTGTGCGCTACTACAACGCCTGGATCGAGC 2034
Db   1463 CACTGCTGTCACGGCTCGCACCGCCACCATGAGACAGTGTGCGCCGCCCCCACCCCAGATTGTGCGCTACTACAACGCCTGGATCGAGC 1522

Qy   2035 GGCACGCAGGACCGGGGACGGGGGAGCGGCAGCCCGGCGAGCGACCCCGGGGACTCTGGGGCCTTGGGCCCCTGGCCAAGG 2094
Db   1523 GGCACGCAGGACCGGGGACGGGGGAGCGGCAGCCCGGCGAGCGACCCCGGGGACTCTGGGGCCTTGGGCCCCTGGCCAAGG 1582

Qy   2095 ATGACCGAGCTGCACGGGCGGCGCGCCCATCCCACCCCATCCTCAGCGACTTCGGGTGAGTGGGACACAGACACACGGCTCAGGCCTGGCAGCGTAGAGG 2154
Db   1583 ATGACCGAGCTGCACGGGCGGCGCGCCCATCCCACCCCATCCTCAGCGACTTCGGGTGAGTGGGACACAGACACACGGCTCAGGCCTGGCAGCGTAGAGG 1642

Qy   2155 CGCCGCGGCGGCGGCCGCCGCCATCCTCAGCGGCGCTCGGGGCGGCTCGGGCAGCGCGCT 2214
Db   1643 CCGCCGGCGGCGGCCGCCGCCATCCTCAGCGGCGCTCGGGGCGGCTCGGGCAGCGCGCT 1702

Qy   2215 CGGCCAGTGCCGCCGGCGGCGGCCGCCGGGGCTCCCAGCGATGACGGCGGATGACGGCGGACG 2274
Db   1703 CGGCCAGTGCCCGCGGCGGCGGCCGCCGGGGCTCCCAGCGATGACGGCGGATGACGGACG 1762
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Qy   2275 AGGACGAGCACGGTGGCGCTTCTTCCCCAGTCCTTCCTCCGCCTGCTTCAGATTCTGAAAGTG 2334
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1763 AGGACGAGCACGGTGGCGGTGGCGGTCTTCCCCAGTCCTTCCTGCCTGCTTCAGATTCTGAAAGTG 1822

Qy   2335 ATATTATCTTTGACAATGAGATGAGAACAGTAAAAGTCAGAATCAGGATGAAGAATTGCA 2394
Db   1823 ATATTATCTTTGACAATGAGATGAGAACAGTAAAAGTCAGAATCAGGATGAAGAATTGCA 1882

Qy   2395 ATGAAAAGAATGGCTGCCATGAAGTGAGCCATCAGTCAGTACGACGAGCTGTGTCACTACC 2454
Db   1883 ATGAAAAGAATGGCTGCCATGAAGTGAGCCATCAGTCAGTACGACGAGCTGTGTCACTACC 1942

Qy   2455 TATACATCCAGATGAGTACTGTGAGAAGAGCACTTACGAGACACTTACGAGACCAGGGAC 2514
Db   1943 TATACATCCAGATGAGTACTGTGAGAAGAGCACTTACGAGACACTTACGAGACCAGGGAC 2002

Qy   2515 TGTATCGAGACACCGTCAGACTCTGGAGGCTTTTCGATGATTCTGATGATTGGATTAGCTT 2574
Db   2003 TGTATCGAGACACCGTCAGACTCTGGAGGCTTTTCGATGATTCTGATGATTGGATTAGCTT 2062

Qy   2575 ATATCCATGAGAAAGGAATGATTCCAGCGGATTTGAAGCCTGTCAACATTTTTTGGATT 2634
Db   2063 ATATCCATGAGAAAGGAATGATTCCAGCGGATTTGAAGCCTGTCAACATTTTTGGATT 2122

Qy   2635 CTGATGACCATGTGAAAAATAGGTGATTTTGGTTTGGGCACAGACCATCTGACGCTTTTTCTG 2694
Db   2123 TTGATGACCATGTGAAAAATAGGTGATTTTGGTTTGGGCACAGACCATCTGACGCCTTTTCTG 2182

Qy   2695 CTGACAGCAAACAAGACGATCAGCAGGAGACTTGATTAAGTCAGAGTCCAAGGAAGCACCAAAT 2754
Db   2183 CTGACAGCAAACAAGACGATCAGCAGGAGACTTGATTAAGTCAGAGTCCAAGGAAGCACCAAAT 2242

Qy   2755 TAACTGGATGGTTGGCACTGCTCTCTATGTAAGCCAGAGTCCAAGGAGTCCAAGGAAGCACCAAAT 2814
Db   2243 TAACTGGATGGTTGGCACTGCTCTCTATGTAAGCCAGAGTCCAAGGAGTCCAAGGAAGCACCAAAT 2302

Qy   2815 CTGCATCAACAACCAGAAAGTGATCTTCTTCAGCCTGGGAATTATCTTCTTTGAGATGTCCT 2874
Db   2303 CTGCATCAACAACCAGAAAGTGATCTTCTTCAGCCTGGGAATTATCTTCTTTGAGATGTCCT 2362

Qy   2875 ATCACCCCATGTGCCGCTTCAGAAAGATCTTGTTCTCCAACCAACTCAGAGATCCCA 2934
Db   2363 ATCACCCCATGTGCCGCTTCAGAAAGATCTTGTTCTCCAACCAACTCAGAGATCCCA 2422

Qy   2935 CTTCGCCTAAGTTCCAGAGACTTTGACGATGGAGAGCGCAAAGAGAAATCAGTCA 2994
Db   2423 CTTCGCCTAAGTTCCAGAGACTTTGACGATGGAGAGCGCAAAGAGAAATCAGTCA 2482

Qy   2995 TCTCCTGGCTGTTGAACCAGATCAGCAGCAACGGCCCACAGCCCACCAGATACTGCTCAAGA 3054
Db   2483 TCTCCTGGCTGTTGAACCAGATCAGCAGCAACGGCCCACAGCCCACCAGAACTGCTCAAGA 2542

Qy   3055 GTGAGCTGCTGCCCCCAGATGGAGAGTCAGCGTCGCATGAGAGTGCTGCACCACA 3114
Db   2543 GTGAGCTGCTGCCCCCAGATGGAGAGTCAGCGTCGCATGAGAGTGCTGCACCACA 2602

Qy   3115 CGGCTGACCAACGTGGATGGGAAGGCCTACCGCACCATGATGGCCCAGATCTTCTCGCGAGC 3174
Db   2603 CGGCTGACCAACGTGGATGGGAAGGCCTACCGCACCATGATGGCCCAGATCTTCTCGCGAGC 2662

Qy   3175 GCATCTTCCCCTGCCATCGATTACGATCGATTACAACCTATGACAGCGGACATTCTTAAAAGAC 3234
Db   2663 GCATCTTCCCCTGCCATCGATTACGATCGATTACAACCTATGACAGCGGACAACTTCTTAAAAGAC 2722

Qy   3235 TCCGTACAGCCAAGATGCAGCAGACATGTGTGAAACCATCATCCGCATCTTTAAAAGAC 3294
Db   2723 TCCGTACAGCCAAGATGCAGCAGACATGTGTGAAACCATCATCCGCATCTTTAAAAGAC 2782

Qy   3295 ATGGAGCTGTCAGTTGTACTCCACTACTGCTTCCCCGAAAACAGACAAATATATGAGC 3354
Db   2783 ATGGAGCTGTTCAGTTGTACTCCACTACTGCTTCCCCGAAAACAGACAAATATATGAGC 2842
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RESULT 8
US-10-425-114-26218
; Sequence 26218, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT: Zhou, Yihua
;  APPLICANT: Kovalic, David K.
;  APPLICANT: Screen, Steven E
;  APPLICANT: Tabaska, Jack E
;  APPLICANT: Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE: 2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26218
;  LENGTH: 4438
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: Clone ID: LIB4117-013-G9_FLI
US-10-425-114-26218
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(Sequence alignment data — paired Qy/Db rows with positional numbering and match bars)

Wed Mar 24 10:54:01 2004   us-09-515-806a-1.rnpb

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Query Match    80.3%;   Score 4436.4;   DB 12;   Length 4438;
Best Local Similarity  100.0%;   Pred. No. 0;
Matches 4437;   Conservative  0;   Mismatches  0;   Indels  1;   Gaps  0;
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Qy    958  CTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTTGTTGTATGAGTGGGTCCTTCAGTGGCAGA  1017
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  CTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTTGTTGTATGAGTGGGTCCTTCAGTGGCAGA    60

Qy   1018  AAAAAATGGGTCATTCCATTCCTTACCAGTCAAGAAAAGAGAAAGAGAAGAAGTGCAAAAAGC  1077
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  AAAAAATGGGTCATTCCATTCCTTACCAGTCAAGAAAAGAGAAAGAGAAGAAGTGCAAAAAGC   120

Qy   1078  AGATTCAAGGAACAGAACAGAATTCAACTCACTGGTAAAATTGAGCCATCCAAATGTAG      1137
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  AGATTCAAGGAACAGAACAGAATTCAACTCACTGGTAAAATTGAGCCATCCAAATGTAG       180

Qy   1138  TACGCTACCTTGCAATGAATCTCAAAGAGCAAGACTCCATCGTGGTGGACATTTAG          1197
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TACGCTACCTTGCAATGAATCTCAAAGAGCAAGACTCCATCGTGGTGGACATTTAG          240

Qy   1198  TGGAGCACATTAGTGGGGTCTCTCTTGCTCGCACACCTCAGGCCCCATCCCTG             1257
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  TGGAGCACATTAGTGGGGTCTCTCTTGCTCGCACACCTCAGGCCCCATCCCTG             300

Qy   1258  TGCATCAGGTTCGCAGGTACACAGCTCAGCTCCTGTGATTATCTGCACAGCA             1317
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  TGCATCAGGTTCGCAGGTACACAGCTCAGCTCCTGTGATTATCTGCACAGCA             360

Qy   1318  ATTCTGTGGTGCATAAGGTCCGAGTGCATCTAATGCTCTGGGATGCAGAAGGCACCG        1377
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ATTCTGTGGTGCATAAGGTCCGAGTGCATCTAATGCTCTGGGATGCAGAAGGCACCG        420

Qy   1378  TCAAGATTACGGACTATAGCATTTCTAAGCGCCTTCGCAGACATTTGCAAGGAGGATGTGT    1437
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  TCAAGATTACGGACTATAGCATTTCTAAGCGCCTTCGCAGACATTTGCAAGGAGGATGTGT    480

Qy   1438  TTGAGCAAACCCGAGTTCGTTTAGTGACAATGCTCTGCCTTATAAAACGGGAAGAAAG      1497
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TTGAGCAAACCCGAGTTCGTTTAGTGACAATGCTCTGCCTTATAAAACGGGAAGAAAG      540

Qy   1498  GAGATGTTTTGGCGTCTTGGCCTTCGTGCTGCTGCTCGTCCTCAGCCAAGGACATGTGGAG   1557
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GAGATGTTTTGGCGTCTTGGCCTTCGTGCTGCTGCTCGTCCTCAGCCAAGGACAATGTGGAG   600

Qy   1558  AGTACCCGTGTGACCAATCCCTGTCAGTGACTTACCAGCTGACTTTCAAGATTTTCTAAAGAAAT 1617
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  AGTACCCGTGTGACCAATCCCTGTCAGTGACTTACCAGCTGACTTTCAAGATTTTCTAAAGAAAT 660

Qy   1618  GTGTGTGCTTGGATGACACAAGGAAAGATGAGTGGAAGAAGACACCAGCTTTA           1677
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  GTGTGTGCTTGGATGACACAAGGAAAGATGAGTGGAAGAAGACACCAGCTTTA           720

Qy   1678  TAAATCCCAGCCAAAATGCCTCAGTGAACAAGTCCTGAACAAGTCTGGAGGACAAG       1737
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  TAAATCCCAGCCAAAATGCCTCAGTGAACAAGTCCTGAACAAGTCTGGAGGACAAG       780

Qy   1738  ATTATGTTGAGACTGTTATTCCTGATACTTCATTGAGTTGAAGAATTACAACTTCTTGGTAAAG  1797
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  ATTATGTTGAGACTGTTATTCCTGATACTTCATTGAGTTGAAGAATTACAACTTCTTGGTAAAG  840

Qy   1798  CACAGAGACAGTTTCCCATCAACCCCATCAACCCGGCCAGCCCGGCGCCCAGCCAGTGA      1857
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CACAGAGACAGTTTCCCATCAACCCCATCAACCCGGCCAGCCCGGCGCCCAGCCAGTGA      900

Qy   1858  GAGCTTTTGGAGCTGTCATCAAGGTGCAAACAGTTGACACGGCTGCTACGCACAGTGA     1917
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  GAGCTTTTGGAGCTGTCATCAAGGTGCAAACAGTTGACACGGCTGCTACGCACAGTGA     960

Qy   1918  AGCGCATCCCCATCAACCCCATCAACCCGGCCAGTTCCGCGGATCAAGGGCGAGTGGACAC   1977
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  AGCGCATCCCCATCAACCCCATCAACCCGGCCAGTTCCGCGGATCAAGGGCGAGTGGACAC  1020

Qy   1978  TGCTGTCACGGCTGCACCATAGAACATTGTGCGCTACTACAACGGCCCTGGATCGAGGCGGC  2037
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  TGCTGTCACGGCTGCACCATAGAACATTGTGCGCTACTACAACGGCCCTGGATCGAGGCGGC  1080
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Qy   2038  ACGAGCGGCCGGCCGGGGAGAGGCGGGCAGCGGCCGGCGGCCGGCAGCGGCCTGGACAGACGGCCG  2097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  ACGAGCGGCCGGCCGGGGAGAGGCGGGCAGCGGCCGGCGGCCGGCAGCGGCCTGGACAGACGGCCG  1140

Qy   2098  ACCGAGCTGCACGCGGCAGCCGGCGAGCGACAGCAGCGACCAGACGGCACTTCGGCGGAGCGCTCGG  2157
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  ACCGAGCTGCACGCGGCAGCCGGCGAGCGACAGCAGCGACCAGACGGCACTTCGGCGGAGCGCTCGG  1200

Qy   2158  CCGCGCCGCACCCATCCTCAGCAGCTTCGGGTGAGTGAGCACTTCGGCGGAGCGCGACGACGAGG  2217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CCGCGCCGCACCCGCCACCGGCTTCGGGTGAGTGAGCACTTCGGCGGAGCGCGACGACGAGG      1260

Qy   2218  CCAGTGCCCGTTTCCCCGGGTCTTCCTCCGCTCCTGCTGTTTCAGATTCTGAAAGTGATA        2277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  CCAGTGCCCGTTTCCCCGGGTCTTCCTCCGCTCCTGCTGTTTCAGATTCTGAAAGTGATA        1320

Qy   2278  ACGAGCACGTGGCGTACTGTGAGAAGAGCACTTTACGAGATCAGAATCAGATTGAAGATTGCAATG  2337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ACGAGCACGTGGCGTACTGTGAGAAGAGCACTTTACGAGATCAGAATCAGATTGAAGATTGCAATG  1380

Qy   2338  TTATCTTTGACAATGAAGATGAGAACAGTGAAGACAGTGAAGATGAAGATTGCAATG          2397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  TTATCTTTGACAATGAAGATGAGAACAGTGAAGACAGTGAAGATGAAGATTGCAATG          1440

Qy   2398  AAAGAAATGCTGCCATGAAAGTGAGCCATCAGTGACAGTGTGCACTACCTAT           2457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  AAAGAAATGCTGCCATGAAAGTGAGCCATCAGTGACAGTGTGCACTACCTAT           1500

Qy   2458  ACATCCAGATGGAGTACTGTGAGAAGAGCACTTACGAGAGACACCATTGACCAGGGACTGT     2517
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  ACATCCAGATGGAGTACTGTGAGAAGAGCACTTACGAGAGACACCATTGACCAGGGACTGT     1560

Qy   2518  ATCGAGACACCGTCAGACTCCGGAGGCTTTTCGAGAGATTCTGGATGGATTAGCTATA        2577
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  ATCGAGACACCGTCAGACTCCGGAGGCTTTTCGAGAGATTCTGGATGGATTAGCTTATA       1620

Qy   2578  TCCATGAGAAGGAATGAATGATTCACCGGGATTGAAGCTTGCACACATTTTTTGGATTCTG     2637
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  TCCATGAGAAGGAATGAATGATTCACCGGGATTGAAGCTTGCACACATTTTTTGGATTCTG     1680

Qy   2638  ATGACCATGTGAAAATAGGTGATTTTGGTTGGCAGACACCATCTAGCCTTTTCTGCTG       2697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  ATGACCATGTGAAAATAGGTGATTTTGGTTGGCAGACACCATCTAGCCTTTTCTGCTG       1740

Qy   2698  ACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAAGAGTCCAAGGAGCACCAAATCTG  2757
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  ACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAAGAGTCCAAGGAGCACCAAATCTG  1800

Qy   2758  CTGGGATGGTTGGACTGCTCTCATGTAAGCCTGGAATTATCTTCTTGAGATGTCCATC        2817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  CTGGGATGGTTGGACTGCTCTCATGTAAGCCTGGAATTATCTTCTTGAGATGTCCATC        1860

Qy   2818  CATACAACCAGAAGTGGATCTCAGAAGGATCCAACTCAGTGTTCTCAACCAAATCTG        2877
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  CATACAACCAGAAGTGGATCTCAGAAGGATCCAACTCAGTGTTCTCAACCAAATCATC        1920

Qy   2878  ACCCCATGGTCACGGCTTCAGGAAAGCAGCATCCCACTT                         2937
           ||||||||||||||||||||||||||||||||||||||
Db   1921  ACCCCATGGTCACGGCTTCAGGAAAGCAGCATCCCACTT                         1980

Qy   2938  CGCCTAAGTTTCAGAGACTTGACGATGGAGCATGCAAAGCAGAAATCAGTCATCT        2997
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  CGCCTAAGTTTCAGAGACTTGACGATGGAGCATGCAAAGCAGAAATCAGTCATCT        2040

Qy   2998  CCTGGCTGTTGAACCACGATCCAGCAAACGGCCACAGCCCAGAACTGCTCAAGAGTG       3057
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  CCTGGCTGTTGAACCACGATCCAGCAAACGGCCACAGCCCAGAACTGCTCAAGAGTG       3100

Qy   3058  AGCTGCTGCCCCCAGCCCAGATGAGAGCTCGATGAAGTGCTGCTCACCACGCGGC        3117
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2037  AGCTGCTGCCCCCAGCCCAGATGAGAGCTCGATGAAGTGCTGCTCACCACGCGGC
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Left column (Db = top line, Qy = bottom line)

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Db  2101 AGCTGCTGCCCCACCCCAGATGGAGAGTCAGAGCTGCATGAGAGTGCTGACCACCACGC  2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3118 TGACCAACGTGGATGGGAAGGCCTACCGGCACCGGACCATGATGGCCCAGATCTTCTCG  3177

Db  2161 TGACCAACGTGGATGGGAAGGCCTACCGGCACCGGACCATGATGGCCCAGATCTTCTCG  2220
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Qy  3178 TCTCCCTGCCATCGATTACACCTATGACAGCGACATACTGAAGGGCAACTTCTCAATCC  3237

Db  2221 TCTCCCTGCCATCGATTACACCTATGACAGCGACATACTGAAGGGCAACTTCTCAATCC  2280
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Qy  3238 GTACAGCCAAGATGCAGCAGCATGTGTGAAACCATCATCCGCATCTTAAAGAGACATG   3297

Db  2281 GTACAGCCAAGATGCAGCAGCATGTGTGAAACCATCATCCGCATCTTAAAGAGACATG   2340
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Qy  3298 GAGCTGTTCAGTTGTGTACTCCACTACCTGCTCCCCGAAACAGACACAAATATGAGCACA 3357

Db  2341 GAGCTGTTCAGTTGTGTACTCCACTACCTGCTCCCCGAAACAGACACAAATATGAGCACA 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3358 ACGAAGCTGCCTATTCAATGGACCACCACAGCGGGGATGCGTGGTGATGCTTCCTTTTGACCTGC 3417

Db  2401 ACGAAGCTGCCTATTCAATGGACCACCACAGCGGGGATGCGTGGTGATGCTTCCTTTTGACCTGC 2460
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Qy  3418 GGATCCCTTTGCAAGATAATGTGGGCAAGAATAATATATATAATTAAACGATACTGCA  3477

Db  2461 GGATCCCTTTGCAAGATAATGTGGGCAAGAATAATATATATAATTAAACGATACTGCA  2520
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Qy  3478 TAGAACGTGTGTTCAGGCCGCGCAAGTTAGATCGATTTCATCCCAAAGACTTCTGGAGT 3537

Db  2521 TAGAACGTGTGTTCAGGCCGCGCAAGTTAGATCGATTTCATCCCAAAGACTTCTGGAGT 2580
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Qy  3538 GTGCATTGATATTGTCACTTCTACCACCAACAGTTTCTGCCACTGCTGAAATTATCT   3597

Db  2581 GTGCATTGATATTGTCACTTCTACCACCAACAGTTTCTGCCACTGCTGAAATTATCT   2640
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Qy  3598 ACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAGAAATTACCAGTATTT 3657

Db  2641 ACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAGAAATTACCAGTATTT 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3658 ATTTGAACCATACCATGTGTATTGAAAGCAATACTCTTACACTGTTGGGATCCCAGAAGATA 3717

Db  2701 ATTTGAACCATACCATGTGTATTGAAAGCAATACTCTTACACTGTTGGGATCCCAGAAGATA 2760
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Qy  3718 AACTCAGTCAAGTCTACACATTATTCTGTATGATGCTGTGACAGAGAAGCTGACGAGGAGAG 3777

Db  2761 AACTCAGTCAAGTCTACACATTATTCTGTATGATGCTGTGACAGAGAAGCTGACGAGGAGAG 2820
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Qy  3778 AAGTGGAAGCTAAATTTGTAATCGTCTTTGTCTTCTAATAGTCTGTGTGACTCTACA  3837

Db  2821 AAGTGGAAGCTAAATTTGTAATCGTCTTTGTCTTCTAATAGTCTGTGTGACTCTACA  2880
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Qy  3838 AGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAATAAATTCATTAATAA 3897

Db  2881 AGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAATAAATTCATTAATAA 2940
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Qy  3898 AACAGAAAACAGGTCAAGACAGTATTGCACAGTTGTGGCTTAAAAGACCTAGAGGAGGTTG 3957

Db  2941 AACAGAAAACAGGTCAAGACAGTATTGCACAGTTGTGGCTTAAAAGACCTAGAGGAGGTTG 3000
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Qy  3958 TTGGACTTGTTGAAGAAACTCGGCCATCAAGTCGAATCATCTTCCAGTTGTGGCTTCATCAAACGAAGGC 4017

Db  3001 TTGGACTTGTTGAAGAAACTCGGCCATCAAGTCGAATCATCTTCCAGTTGTGGCTTCATCAAACGAAGGC 3060
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Qy  4018 ACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTGTGGCTTCATCAAACGAAGGC  4077

Db  3061 ACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTGTGGCTTCATCAAACGAAGGC  3120
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Qy  4078 AAAGGGGCTGTACCTGAAATCCTCGAGCTGATATGAACCAGATACCTGCTGATTCCCCAGT 4137

Db  3121 AAAGGGGCTGTACCTGAAATCCTCGAGCTGATATGAACCAGATACCTGCTGATTCCCCAGT 3180
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Qy  4138 TTAGAGGGCCACAAGCTCTGGGGCCCAGTTCCCACTGCCAGTTCAGCAGTCAGCATAGTCATATAG 4197

Db  3181 TTAGAGGGCCACAAGCTCTGGGGCCCAGTTCCCACTGCCAGTTCAGCAGTCAGCATAGTCATATAG 3240
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Right column (Qy = top line, Db = bottom line)

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Qy  4198 ACAAGAGATATCTGCTGCTGTCCTCAACATGGAGGAATCTGTTACAATAAGCTCTTGTGACC 4257
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Db  3241 ACAAGAGATATCTGCTGCTGTCCTCAACATGGAGGAATCTGTTACAATAAGCTCTTGTGACC 3300

Qy  4258 TCCTGGTTGTAAGTGTTGGTCAGATGTCTATGTCAGGGCCATCAACTCAACCTACCCAGAAAC 4317
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 TCCTGGTTGTAAGTGTTGGTCAGATGTCTATGTCAGGGCCATCAACTCAACCTACCCAGAAAC 3360

Qy  4318 TCTGGACAGCAGGCATCACAGCAGAAATCATGTCGACTGGTCACAGTCCCAAGAGAGGAAT 4377
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Db  3361 TCTGGACAGCAGGCATCACAGCAGAAATCATGTCGACTGGTCACAGTCCCAAGAGAGGAAT 3420

Qy  4378 TACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGTCTCGGATAAAGAAG 4437
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Db  3421 TACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGTCTCGGATAAAGAAG 3480

Qy  4438 GAAGCCATGTCAAGGTTAAGTCTTCGAGAAGGAAAGCAGACAGAGAAGCCGTGTGCTGG 4497
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Db  3481 GAAGCCATGTCAAGGTTAAGTCTTCGAGAAGGAAAGCAGACAGAGAAGCCGTGTGCTGG 3540

Qy  4498 AGACTGAACTGTGGACCATGTACTGCAGAAACTGAGGACTAAAGTCACTGATGAAAGGA 4557
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Db  3541 AGACTGAACTGTGGACCATGTACTGCAGAAACTGAGGACTAAAGTCACTGATGAAAGGA 3600

Qy  4558 ATGGCAGAGAAGCTTCCGATAAATCTTGCAGTGCAAAATCTGAAGGGGTCATTTTCTAATG 4617
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 ATGGCAGAGAAGCTTCCGATAAATCTTGCAGTGCAAAATCTGAAGGGGTCATTTTCTAATG 3660

Qy  4618 CTTCAGGTTTGTTTGAAATCCATGGAGCAACAGTGGTTCCCATTGTGAGTGTCTAGCCC 4677
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Db  3661 CTTCAGGTTTGTTTGAAATCCATGGAGCAACAGTGGTTCCCATTGTGAGTGTCTAGCCC 3720

Qy  4678 CGGAGAAGCTGTCAGCCAGCACTAGGAGCGCTATGAAACTCAGGTACAAACTCGACTTC 4737
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 CGGAGAAGCTGTCAGCCAGCACTAGGAGCGCTATGAAACTCAGGTACAAACTCGACTTC 3780

Qy  4738 AGACCTCCCTTGCCCAACTTACATCAGAAGAAGCAGTGAAATTGAAATTCTGGCTGTGGATC 4797
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Db  3781 AGACCTCCCTTGCCCAACTTACATCAGAAGAAGCAGTGAAATTGAAATTCTGGCTGTGGATC 3840

Qy  4798 TACCCAAAGAACAATATTACAGTTTTATCATTAGAGTGGATGCTGATGAACAGGCAT 4857
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Db  3841 TACCCAAAGAACAATATTACAGTTTTATCATTAGAGTGGATGCTGATGAACAGGCAT 3900

Qy  4858 TTAACAACTGTGAAGCAGCTGCTGTCACGCCTGCCAAAGCAAAGATACCTCAAATTAG 4917
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Db  3901 TTAACAACTGTGAAGCAGCTGCTGTCACGCCTGCCAAAGCAAAGATACCTCAAATTAG 3960

Qy  4918 TCTGTGATGAAATTTATACATCAAAGTAGAAAAAAAGGTGTCTGCATTCTGTGTACA 4977
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Db  3961 TCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAAGGTGTCTGCATTCTGTGTACA 4020

Qy  4978 GCTATAGAGATGACTACTACAGAATCTATTTT AACCCTGAAACTGCGTAACCTCA 5037
         |||||||||||||||||||||||||||||||| ||||||  ||| |||||||||||
Db  4021 GCTATAGAGATGACTACTACAGAATCTATTTTTAACCCTAAAGAACTGTGTTAACCTCA 4080

Qy  5038 TTCAAACAGACAGAGAGGCTTATACTGGAATAATGTTGTACATTCATCATAATTCA 5097
         |||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  4081 TTCAAACAGACAGAGAGGCTTATACTGGAATAATGTTGTACATTCATCATAATTAA 4140

Qy  5098 AATTAAATTCTAAGAGAGAGGCTGGGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTGG 5157
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Db  4141 AATTAAATTCTAAGAGAGAGGCTGGGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTGG 4200

Qy  5158 GAAGCCAAGGCAGGAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCCTGAGCAACAAAG 5217
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Db  4201 GAAGCCAAGGCAGGAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCCTGAGCAACAAAG 4260

Qy  5218 CAAGACCCCATCTCTATAAAAATAAAAATTAGCCGGGCGTGGTGGCACATGCCTGTA 5277
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Db  4261 CAAGACCCCATCTCTATAAAAATAAAAATTAGCCGGGCGTGGTGGCACATGCCTGTA 4320
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Qy   5278 GTCCCAGCTACTCCAGAGGCTGAGATGATCATCTGAGCCTCAGGAGGTTGAGGCTGCAG 5337
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Db   4321 GTCCCAGCTACTCCAGAGGCTGAGATGATCATCTGAGCCTCAGGAGGTTGAGGCTGCAG 4380

Qy   5338 TGAGCTGTGACTGCGCCACTGCACTCCAGTCTGGGACACAGAGCAAGACCCTGTCTT 5395
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Db   4381 TGAGCTGTGACTGCGCCACTGCACTCCAGTCTGGGACAACAGAGCAAGACCCCTGTCTT 4438

RESULT 9
US-09-836-392-6
; Sequence 6, Application US/09836392
; Patent No. US20020173458A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides, a
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT020P1
; CURRENT APPLICATION NUMBER: US/09/836,392
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: PCT/US00/28066
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 60/159,542
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/165,914
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/189,027
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 6
;   LENGTH: 2946
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-836-392-6

Query Match      53.0%;  Score 2928.8;  DB 9;  Length 2946;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 2930;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

Qy   2485 GCACTTACGAGACACCATGACCAGGGACTGATCGAGCACCGTCAGACTTCGGAGGC 2544
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Db     12 GCACTTACGAGACACATTGACCAGGGACTGTATCGAGCACCGTCAGACTTCGGAGGC 71

Qy   2545 TTTTTCGGAGAGATTCGGATGGATTAGCTTATATCCATGAGAAAGGAATGATTCACCGGG 2604
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Db     72 TTTTTCGGAGAGATTCGGATGGATTAGCTTATATCCATGAGAAAGGAATGATTCACCGGG 131

Qy   2605 ATTTGAAGCCTGTCAACATTTTTTGGATTCTGATGACCCATGTGAAAATAGGTGATTTTG 2664
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Db    132 ATTTGAAGCCTGTCAACATTTTTTGGATTCTGATGACCCATGTGAAAATAGGTGATTTTG 191

Qy   2665 GTTTGGCGACAGACCATCCTAGCCTTTTCTCGCTGCAGCAGCAAACAAGACGATCAGACAGGAG 2724
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 GTTTGGCGACAGACCATCCTAGCCTTTTCTCGCTGCAGCAGCAAACAAGACGATCAGACAGGAG 251

Qy   2725 ACTTGATTAAGTCAGACCCTTCAGGTCACTTAACTGGGATGGTTGGCACTCGCTCTCTCTATG 2784
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 ACTTGATTAAGTCAGACCCTTCAGGTCACTTAACTGGGATGGTTGGCACTCGCTCTCTCTATG 311

Qy   2785 TAAGCCCAGAGGTCAAGGAAGCACCAAATCTGCATACAACCAGAAAGTGGATCTCTTCA 2844
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Db    312 TAAGCCCAGAGGTCAAGGAAGCACCAAATCTGCATACAACCAGAAAGTGGATCTCTTCA 371

Qy   2845 GCCTGGGAATTATCTTCTTTGAGATGTCCTATCACCCCATGGTCGACGGGTTCACGGAAAGGA 2904
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 GCCTGGGAATTATCTTCTTTGAGATGTCCTATCACCCCATGGTCGACGGGCTTCACGGAAAGGA 431

Qy   2905 TCTTTGTTCTCAACCAACTCAGAGATCCCACTTCGCCTAAGTTTCCAGAAGACTTTGACG 2964
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Db    432 TCTTTGTTCTCAACCAACTCAGAGATCCCACTTCGCCTAAGTTTCCAGAAGACTTTGACG 491

Qy   2965 ATGGGAGCATGCAAAGCAAGAAATCAGTCAATCTCCTGGCGTGTTGAACCACGATCCAGCAA 3024
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Db    492 ATGGGAGCATGCAAAGCAAGAAATCAGTCAATCTCCTGGCGTGTTGAACCACGATCCAGCAA 551

Qy        AACGGGCCCACAGCCACCAGAGACTGCTCAGAGTGAGTGCTGCTGCCCCCACCCCAGATGGAGG 3084
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Db   3025 AACGGGCCCACAGCCACCAGAGACTGCTCAGAGTGAGTGCTGCTGCCCCCACCCCAGATGGAGG 611

Qy   3085 AGTCAGAGCTGCATGAGAGTGCTGCACCACGTGACCAACGTGGATGGGAAGGCCTACC 3144
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    612 AGTCAGAGCTGCATGAGAGTGCTGCACCACGTGACCAACGTGGATGGGAAGGCCTACC 671

Qy   3145 GCACCATGATGGCCCAGATCTTCGAGCGCATCCCCTGCCATGATTACACCTATG 3204
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Db    672 GCACCATGATGGCCCAGATCTTCGCACGCATCCCCTGCCATCGATTACACCCTATG 731

Qy   3205 ACAGGGACATACTGAAGGGCAACTTCTCAATCCGTAGCAGATGCAGCAGCAGCATGTGT 3264
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Db    732 ACAGGGACATACTGAAGGGCAACTTCTCAATCCGTAGCAGATGCAGCAGCAGCATGTGT 791

Qy   3265 GTGAAACCATCATCCGCATCTTTAAAAGACATGAGCACAACGAGCTGCCCTATTCATGGACCACA 3324
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    792 GTGAAACCATCATCCGCATCTTTAAAAGACATGAGCACAACGAGCTGCCCTATTCATGGACCAC 851

Qy   3325 TGCTTCCCGAAACAGACAAATATGAGCACAAATATGAGACCTGCCGGATCCCTTTGCAAGATATGTGGCAA 3384
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 TGCTTCCCGAAACAGACAAATATGAGCACAAATATGAGACCTGCCGGATCCCTTTGCAAGATATGTGGCAA 911

Qy   3385 GCGGGATGTGGTGATGCTTCCTTTGACCTGCGGATCCCTTTGCAAGATATGTGGCAA 3444
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    912 GCGGGATGTGGTGATGCTTCCTTTGACCTGCGGATCCCTTTGCAAGATATGTGGCAA 971

Qy   3445 GAAATAATATATTGAATTTAAAACGATACTGCATAGAACGTGTGTTGATATTGTCACTTCTACCA 3504
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Db    972 GAAATAATATATTGAATTTAAAACGATACTGCATAGAACGTGTGTTGATATTGTCACTTCTACCA 1031

Qy   3505 TAGATCGATTTCATCCCAAAGAACTTCTGCCCACTGCTGAAATTATCACTATCATGAAATCATCCAAGAGT 3564
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 TAGATCGATTTCATCCCAAAGAACTTCTGGAGTGTGCATTTGATATTGTCACTTCTACCA 1091

Qy   3565 CCAACAGCTTCTGCCCACTGCTGAAATTATCACTATCATGAAATCATCCAAGAGT 3624
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Db   1092 CCAACAGCTTCTGCCCACTGCTGAAATTATCACTATCATGAAATCATCCAAGAGT 1151

Qy   3625 TTCCAGCACTTCAGGAAGAAATTACAGTATTATTTGAACCATACCATGTGTTATTGAAAG 3684
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Db   1152 TTCCAGCACTTCAGGAAGAAATTACAGTATTATTTGAACCATACCATGTGTTATTGAAAG 1211

Qy   3685 CAATACTCTTACACTGTGGGATCCTGATGACCATGTGAAAATAGTGATTTTG 3744
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Db   1212 CAATACTCTTACACTGTGGGATCCTGATGACCATGTGAAAATAGTGATTTTG 1271

Qy   3745 ATGATGCTGTGACAGAGAGCTGACGAGGAGAAGCTGAAGCTAAATTTTGTAATCTGT 3804
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 ATGATCGTGTGACAGAGAGCTGACGAGGAGAAGCTGAAGCTAAATTTTGTAATCTGT 1331

Qy   3805 CTTTGTCTTCTAATAGTCTGTGTCTAATGTCTGTGTGCTCCTCACAGTTATTGAACAGAGGAGGATTGC 3864
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Db   1332 CTTTGTCTTCTAATAGTCTGTGTCTAATGTCTGTGTGCTCCTCACAGTTATTGAACAGAGGAGGATTTGC 1391

Qy   3865 AAGATCTTATGCCAACAATAAATTCATTAATAAAACAGGTAGTTGCACAGTTGG 3924
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Db   1392 AAGATCTTATGCCAACAATAAATTCATTAATAAAACAGGTAGTTGCACAGTTGG 1451

Qy   3925 TGAAGTATGGCTTAAAGACCTAGAGAGAGTTGTTGGACTGTTGAAGAAACTCGGCATCA 3984
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Db   1452 TGAAGTATGGCTTAAAGACCTAGAGAGAGTTGTTGGACTGTTGAAGAAACTCGGCATCA 1511

Qy   3985 AGTTACAGGTCTTGATCAATTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCA 4044
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1512 AGTTACAGGTCTTGATCAATTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCA 1571

Qy   4045 TCTTTCCAGTTGTGTGCTTCATCAAACGAAGGCAAAGGCAAAATCCTCGCACG 4104
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        TCTTTCCAGTTGTGTGCTTCATCAAACGAAGGCAAAGGCAAAATCCTCGCACG
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Query Match      38.8%;  Score 2144.6;  DB 9;  Length 2200;
Best Local Similarity   99.0%;  Pred. No. 0;
Matches 2173;  Conservative  2;  Mismatches  16;  Indels  3;  Gaps  2;
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Qy  5185 ACCAGGAGTTTGAGACCGCTGAGCAACAAAGCAAGACCCATCTCTATAAAACTAAA 5244
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Db  2712 ACCAGGAGTTTGAGACCAGCCTGAGCAACAACAAGCAAGACCCATCTCTATAAAAACTAAA 2771

Qy  5245 AAAATTAGTTGGGCATGGTGGCACATGGCCTGTAGTCCTCCAGAGGCTGAGATG 5304
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2772 AAAATTAGTTGGGCATGGTGGCACATGGCCTGTAGTCCTCCAGAGGCTGAGATG 2831

Qy  5305 GATCATCTGAGCCTCAGGAGTTGAGGCTGCAGTGAGCTGTGACTGCGCCACTGCACTCC 5364
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2832 GATCATCTGAGCCTCAGGAGTTGAGGCTGCAGTGAGCTGTGACTGCGCCACTGCACTCC 2891

Qy  5365 AGTCTGGGACAACAGAGCAAGACCCTGTCTTAAAAAAAAAGAAAAAAAA 5416
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Db  2892 AGTCTGGGACAACAGAGCAAGACCCTGTCTTAAAAAAAAAAAAAAAAAA 2943
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Db  1572 TCTTCCAGTTGTGGCTTCATCAAACGAAGGCAAAGGGCTGTGACCTGAAATCCTCGCAG 1631

Qy  4105 CTGGAGGCAGATATGACCTGCTGATCCCAGTTTAGAGGGGCCACAAGCTCTGGGGCCAG 4164
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1632 CTGGAGGCAGATATGACCTGCTGATCCCAGTTTAGAGGGGCCACAAGCTCTGGGGCCAG 1691

Qy  4165 TTCCCACTGCCATTGGGGTCAGCATAGCTATAGACAAGATATCTGCTGCTGTCCTCAACA 4224
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1692 TTCCCACTGCCATTGGGGTCAGCATAGCTATAGACAAGATATCTGCTGCTGTCCTCAACA 1751

Qy  4225 TGGAGGAATCGTTACAATAAGCTCTTGTGACCTCCTGGTTGTAAGTGTTGTCAGATGT 4284
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1752 TGGAGGAATCGTTACAATAAGCTCTTGTGACCTCCTGGTTGTAAGTGTTGTCAGATGT 1811

Qy  4285 CTATGTCCAGGGCCATCAACAACCTAACCCAGAAACTCTGGACAGCAGGCATCACAGACGAAA 4344
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Db  1812 CTATGTCCAGGGCCATCAACAACCTAACCCAGAAACTCTGGACAGCAGGCATCACAGACGAAA 1871

Qy  4345 TCAATGTACGACTGGTCAACAGTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAA 4404
         ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1872 TCATGTACGACTGGTCACAGTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAA 1931

Qy  4405 TCAACTTAGTGGCCCTTGTCTCGGATAAAGAACGGAAGCCATGTCAAGGTTAAGTCTTTCG 4464
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Db  1932 TCACCTATGTGGCCCTTGTCTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTCG 1991

Qy  4465 AGAAGGAAAGGCAGACAGAGAAGCGTGTGCTGGAGACTGAACTTGTTGGACCATGTACTGC 4524
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1992 AGAAGGAAAGGCAGACAGAGAAGCGTGTGCTGGAGACTGAACTTGTTGGACCATGTACTGC 2051

Qy  4525 AGAAACTGAGGACTAAAGTCACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTG 4584
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Db  2052 AGAAACTGAGGACTAAAGTCACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTG 2111

Qy  4585 CAGTGCAAAATCTGAAGGGGTCATTTCTAATGCTTCAGGTTTGTTGAAATCCATGGAG 4644
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Db  2112 CAGTGCAAAATCTGAAGGGGTCATTTCTAATGCTTCAGGTTTGTTGAAATCCATGGAG 2171

Qy  4645 CAACAGTGGTTCCCATTGTGAGTGTGCTAGCCCCGGAGAAGCTGTCAGCCAGCACTAGGA 4704
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2172 CAACAGTGGTTCCCATTGTGAGTGTGCTAGCCCCGGAGAAGCTGTCAGCCAGCACTAGGA 2231

Qy  4705 GGGCCTATGAAACTCAGGTACAAACTCGACTTCAGACCTCCCTGCCAACTTACATCAGA 4764
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Db  2232 GGGCCTATGAAACTCAGGTACAAACTCGACTTCAGACCTCCCTGCCAACTTACATCAGA 2291

Qy  4765 AAAGCAGTGAAATTGAAATTCTGGCTGTGTGGGATCTCACCCAAAGAAACAATATTACAGTTTT 4824
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Db  2292 AAAGCAGTGAAATTGAAATTCTGGCTGTGTGGGATCTCACCCAAAGAAACAATATTACAGTTTT 2351

Qy  4825 TATCATTAGAGTGGGATGCTGATGAAACAGGCATTTAACACAACTGTGAAGCAGCTCTGT 4884
         |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  2352 TATCATTAGAGTGGGATGCTGATGAACAGGCATTTAACACAACTGTGAAGCAGCTCTGT 2411

Qy  4885 CACGGCCTGCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAG 4944
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Db  2412 CACGGCCTGCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAG 2471

Qy  4945 TAGAAAAAAGGTGTCTGTGCTATTTCTGTACAGGCTATAGCTATAGACGATGACTACTACAGAATCT 5004
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2472 TAGAAAAAAGGTGTCTGTGCTATTTCTGTACAGCTATAGCTATAGACGATGACTACTACAGAATCT 2531

Qy  5005 TATTTTAACCCTAAAGAACTGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGA 5064
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Db  2532 TATTTTAACCCTAAAGAACTGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGA 2591

Qy  5065 ATAATGGAATGTTGTACATTCATCATCATAATTAAAATTAAATTCTAAGAAGAGGCTGGGTG 5124
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2592 ATAATGGAATGTTGTACATTCATCATCATAATTAAAATTAAATTCTAAGAAGAGGCTGGGTG 2651

Qy  5125 CAGTGGCTCACACCTTAATCCCAGCACTTTGGGAAGGCCAAGGCAGGACTGCTTGAA 5184
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Db  2652 CAGTGGCTCACACCTTAATCCCAGCACTTTGGGAAGGCCAAGGCAGGACTGCTTGAA 2711
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Qy  3206 CAGCGACATACTGAAGGCAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTG 3265
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Db     9 CAGCGACACTACTGAAGGCAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTG 68

Qy  3266 TGAAACCATCATCCGCATCTTAAAAGACATGGAGCTGTTCAGTTGTACTCCACTACT 3325
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Db    69 TGAAACCATCATCCGCATCTTAAAAGACATGGAGCTGTTCAGTTGTACTCCACTACT 128

Qy  3326 GCTTCCCCGAAACAGACAAATATGAGCAACGAAGCTGCCCATTCATGGACCACCAG 3385
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Db   129 GCTTCCCCGAAACAGACAAATATGAGCAACGAAGCTGCCCATTCATGGACCACCAG 188

Qy  3386 CGGGATGCTGGTGATGCTTCCTTTGACCTGCGGATCCCTTTGCAAGATATGTGGCAAG 3445
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Db 1269 GAAGGAAAGGCAGACAGAGAAGGCTGTGTCTGGAGACTGAACTTGTGGACCATGTACTGCA 1328
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Qy 4526 GAAACTGAGGACTAAAGTCACTGATGAGAAAGGAATGGCAGAGAGAGCTTCCGATAATCTGC 4585
Db 1329 GAAACTGAGGACTAAAGTCACTGATGAGAAAGGAATGGCAGAGAGAAGCTTCCGATAATCTTGC 1388

Qy 4586 AGTGCAAAATCTGAAGGGGTCATTTTCTAATGCTTCAGGTTTGTTTGAAATCCATGGAGC 4645
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Db 1389 AGTGCAAAATCTGAAGGGGTCATTTTCTAATGCTTCAGGTTTGTTTGAAATCCATGGAGC 1448

Qy 4646 AACAGTGGTTCCCATTGTGAGTGTGCTAGCCCCGGGAAGTCGTCAGCCAGCACTAGGAG 4705
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1449 AACAGTGGTTCCCATTGTGAGTGTGCTAGCCCCGGGAAGTCGTCAGCCAGCACTAGGAG 1508

Qy 4706 GCGCTATGAAACTCAGGTACAAACTCGACTTCAGAACCTCCCTGCCAACTTACATCAGAA 4765
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Db 1509 GCGCTATGAAACTCAGGTACAAACTCGACTTCAGAACCTCCCTGCCAACTTACATCAGAA 1568

Qy 4766 AAGCAGTGAAATTGAAATTCTGGCTGTGGATCTCACCCAAAGAAACAATATTACAGTTTTT 4825
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Db 1569 AAGCAGTGAAATTGAAATTCTGGCTGTGGATCTCACCCAAAGAAACAATATTACAGTTTTT 1628

Qy 4826 ATCATTAGAGTGGGATGCTGATGAACAGCATTAACACAACTGTGAAGCAGCTGCTGTC 4885
          ||||||||||||||| ||||||||||||||||||||| |||||||||||||||||
Db 1629 ATCATTAGAGTGGGATGCTGATGAACAGCATTAACACAACTGTGAAGCAGCTGCTGTC 1688

Qy 4886 ACGCCTGCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGT 4945
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Db 1689 ACGCCTGCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGT 1748

Qy 4946 AGAAAAAAAGTGTCTGTTGCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTT 5005
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Db 1749 AGAAAAAAAGTGTCTGTTGCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTT 1808

Qy 5006 ATTTTAACCCTAAAGAACTGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGAA 5065
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Db 1809 ATTTTAACCCTAAAGAACTGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGAA 1868

Qy 5066 TAATGGAATGTGTACATTCATCATAATTAAAATTAAAATTAAAATTCTAAGAGAGGCTGGGTGC 5125
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Qy 5126 AGTGGCTCACACCTTTAATCCCAGCACTTTGGGAAGCCAAGGCAGGAGGACTGCTTGAAA 5185
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Db 1929 AGTGGCTCACACCTTTAATCCCAGCACTTTGGGAAGCCAAGGCAGGAGGAAGACTGCTTGAAA 1988

Qy 5186 CCAGGAGTTTGAGACCAGCCTGAGCAACAAAGCAAGACCCCATCTCTATAAAAACTAAAA 5245
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Db 1989 CCAGGAGTTTGAGACCAGCCTGAGCAACAAAGCAAGACCCCATCTCTATAAAAACTAAAA 2048

Qy 5246 AAATTAGTTGGGCATGGTGGCACATGCCTGTAGTCCCAGCTACTCCAGAGGCTGAGATGG 5305
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Db 2049 AAATTAGTTGGGCATGGTGGCACATGCCTGTAGTCCCAGCTACTCCANAGGCTGAGATGG 2108

Qy 5306 ATCATCTGAGCCTCAGGAGGTTGAGCCTGCAGTGAGCTGCGCCCACTGCACTCCA 5365
          ||||||||||||||||||||||||||||||||| || ||||||||| ||||||| || ||||
Db 2109 ATCATCTGAGCCTCAGGAGGTTGACGCTGCANTGA-CTGTGACTGCGCGCCNCTG--ACTCC 2165

Qy 5366 GTCTGGGACAACAGAGCAAGACCCTGTCTTAAAA 5399
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Db 2166 ATCTGGGCAACAGANCANGACCCTGCTTAAATA 2199

RESULT 11
US-10-006-285-498
; Sequence 498, Application US/10006285
; Publication No. US20030165854A1
; GENERAL INFORMATION:
; APPLICANT: Mary Jane Cunningham
; APPLICANT: Matthew R. Kaser
; TITLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS
; FILE REFERENCE: PA-0039 US
; CURRENT APPLICATION NUMBER: US/10/006,285

Qb 189 CGGGATGCTGGTGATGCTTCCTTTGACCTGCGGATCCCTTTGCAAGATATGTGGCAAG 248
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Qy 3446 AAATAATATATTGAATTAAAACGATACTGCATAGAACGTGTGTTCAGGCCGCGCAAGTT 3505
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Db 249 AAATAATATATTGAATTAAAACGATATTGCATAGAACGTGTGTTCAGGCCGCGCAAGTT 308

Qy 3506 AGATCGATTTCATCCCAAAGAACTTCTGGAGTGTGCATTTGATATGTCACTTCTACCAC 3565
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Db 309 AGATCGATTTCATCCCAAAGAACTTCTGAGTGTGCATTTGATATGTCACTTCTACCAC 368

Qy 3566 CAACAGCTTTCTGCCCACTGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTT 3625
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Db 369 CAACAGCTTTCTGCCCACTGCTGAAATTATCTACACCATCATCTATGAAATCATCCAAGAGTT 428

Qy 3626 TCCAGCACTTCAGGAAAGAGAAATTACAGTATTTATTGAACCATACCATGTTATTGAAAGC 3685
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Db 429 TCCCAGCACTTCAGGAAAGAGAAATTACAGTATTTATTGAACCATACCATGTTATTGAAAGC 488

Qy 3686 AATACTCTTACACTGTGGGATCCCAGAAGATAAACTCAGTCAAGTCACATTATTCTGTA 3745
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Qy 3746 TGATGCTGTGACAGAGAAGCTGACGAGGAGAAGTGGAAGCTAAATTTGTAATCTGTC 3805
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Db 549 TGATGCTGTGACAGAGAAGCTGACGAGGAGAAGTGGAAGCTAAATTTGTAATCTGTC 608

Qy 3806 TTTGTCTTCTAATAGTCTGTGTCGACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCA 3865
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Db 609 TTTGTCTTCTAATAGTCTGTGTCGACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCA 668

Qy 3866 AGATCTTATGCCAACAATAAATTCATTAATAAAACAGAAAAACAGGTATTGCACAGTTGGT 3925
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Qy 3926 GAAGTATGGCTTAAAAGACCTAGAGGAGGTTGTTGGACTGTTGAGAAACTCGGCATCAA 3985
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Db 729 GAAGTATGGCTTAAAAGACCTAGAGGAGGTTGTTGGACTGTTGAGAAACTCGGCATCAA 788

Qy 3986 GTTACAGGTCTTGATCAATTGGGCTTGGTTTACAAGGTGCAGCAGCAATGGAATCAT 4045
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Db 789 GTTACAGGTCTTGATCAATTGGGCTTGGTTTACAAGGTGCAGCAGCAATGGAATCAT 848

Qy 4046 CTTCCAGTTTGTGGCTTCATCAAACGAAGGCAAAGGGCTGTACCTGAAATCCTCGCGAGC 4105
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Db 849 CTTCCAGTTTGTGGCTTCATCAAACGAAGGCAAAGGGCTGTACCTGAAATCCTCGCGAGY 908

Qy 4106 TGGAGGCAGATATGACCTGCTGATTCCCCAGTTTGAGGGGGCCACAAGCTCTGGGGCCAGT 4165
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Db 909 TGGAGGCAGATATGACCTGCTGATTCCCCAGTTTGAGGGGGCCACAAGCTCTGGGGCCAGT 968

Qy 4166 TCCCACTGCCATTGGGGTCAGCATAGCTATAGACAAGAATATCTGCTGTCTCCTCACAT 4225
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Db 969 TCCCACTGCCATTGGGGTCAGCATAGCTATAGACAAGAATATCTGCTGTCTCCTCACAT 1028

Qy 4226 GGAGGAATCTGTTACAATAAGCTCTTGTGACCTCCTGGTTGTAAGTGTTGGTCAGATGTC 4285
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Db 1029 GGAGGAATCTGTTACAATAAGCTCTTGTGACCTCCTGGTTGTAAGTKTTGGTCAGATGTC 1088

Qy 4286 TATGTCCAGGGCCATCAAACTTAACCCAGAAACTCTGGACAGAGGCATCACAGCAGAAAT 4345
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Db 1089 TATGTCCAGGGCCATCAAACTTAACCCAGAAACTCTGGACAGCAGGCATCACAGCAGAAAT 1148

Qy 4346 CATGTACGACTGGTCACAGTCCCAAGAGGAATTACAAGAGTACTCGACATCATGAAAT 4405
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Db 1149 CATGTACGACTGGTCACAGTCCCAAGAGGAATTACAAGAGTACTCCAGACATCATGAAAT 1208

Qy 4406 CACCTTATGTGGCCCTTGTCTCGGATAAAGAAGGAGAGCCATGCAAGGTTAAGTCTTTCGA 4465
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Qy 4466 GAAGGAAAGGCAGACAGAGAAGGCTGTGTCTGGAGACTGAACTTGTGGACCATGTACTGCA 4525
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CURRENT FILING DATE:   2001-12-05
NUMBER OF SEQ ID NOS:  514
SOFTWARE: PERL Program
SEQ ID NO 498
LENGTH: 1845
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030165854A1 1099669.1
NAME/KEY: unsure
LOCATION: 467, 528, 540
OTHER INFORMATION: a, t, c, g, or other

US-10-006-285-498

Query Match      31.1%;   Score 1716.4;   DB 14;   Length 1845;
Best Local Similarity   94.0%;
Matches 1841;   Conservative   0;   Mismatches   0;   Indels   4;   Gaps   1;
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Qy   3157 CCCAGATCTTCTGCAGGCATCTCCCTGCCATCGATTACACCTATGACAGCGACATAC 3216
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Db      1 CCCAGATCTTCTGCAGCGCATCTCCCTGCCATCGATTACACCTATGACAGCGACATAC 60

Qy   3217 TGAAGGGCAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGAAACCATCA 3276
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Db     61 TGAAGGGCAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGAAACCATCA 120

Qy   3277 TCCGCATCTTTAAAAGACATGGAGCTGTTCAGTTGTGTACTCCACTACTGCTTCCCGAA 3336
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Db    121 TCCGCATCTTTAAAAGACATGGAGCTGTTCAGTTGTGTACTCCACTACTGCTTCCCGAA 180

Qy   3337 ACAGACAAATATATGAGCACAACGAAGCTGCCCTATTCATGGACCACCAGCGGGATGCTGG 3396
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Db    181 ACAGACAAATATATGAGCACAACGAAGCTGCCCTATTCATGGACCACCAGCGGGATGCTGG 240

Qy   3397 TGATGCTTCCTTTGACCTGCGGATCCCTTTGCAAGATATGTGGCAAGAAATAATATAT 3456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGATGCTTCCTTTGACCTGCGGATCCCTTTGCAAGATATGTGGCAAGAAATAATATAT 300

Qy   3457 TGAATTTAAAACGATACTGCATGAACGTGTGTTCAGGCCGGCCAAGTTAGATCGATTTC 3516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGAATTTAAAACGATACTGCATGAACGTGTGTTCAGGCCGGCCAAGTTAGATCGATTTC 360

Qy   3517 ATCCCAAAGAACTTCTGGAGTGTGCATTGATATTGTCACTTCTACCACCAACAGCTTTC 3576
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Qy   3577 TGCCCACTGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTC 3636
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Db    421 TGCCCACTGCTGAAATTATCTACACTATCTATGAAATCATCCAAGANTTTCCAGCACTTC 480

Qy   3637 AGGAAAGAAATTACAGTATTATTTATTGAACCATGTATTGAAAGCAATACTACTTAC 3696
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Db    481 AGGAAAGAAATTACAGTATTATTTATTGAACCATGTATTGAAANCAATACTACTTAN 540

Qy   3697 ACTGTGTGGATCCCAGAGAATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGA 3756
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Db    541 ACTGTGTGGGATCCCAGAGAATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGA 600

Qy   3757 CAGAGAAGCTGACGAGGAGTGGAAGCTAAATTTGTAATCTGTTCTTTGTCTTCTA 3816
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Db    601 CAGAGAAGCTGACGAGGAGTGGGAAGCTAAATTTGTAATCTGTTCTTTGTCTTCTA 660

Qy   3817 ATAGTCTGTGCGACTCTACAAGTTTATTGAACAGAGGGAGATTGCAAGATCTTATGC 3876
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATAGTCTGTGCGACTTCTACAAGTTTATTGAACAGAGGGAGATTGCAAGATCTTATGC 720

Qy   3877 CAACAATAAAATTCATTTAATAAAACAGAAAAACAGGTATTGCACAGTTGGTGAAGTATCGGCT 3936
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAACAATAAAATTCATTTAATAAAACAGAAAAACAGGTATTGCACAGTTGGTGAAGTATCGGCT 780

Qy   3937 TAAAAGACCTAGAGGAGGAGGTTGTTGGACTGTTGAAGAAACTCGGCATCAAGTTACAGGTCT 3996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TAAAAGACCTAGAGGAGGAGGTTGTTGGACTGTTGAAGAAACTCGGCATCAAGTTACAGGTCT 840
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Qy   3997 TGATCAATTTGGGCTTGGTTTACAAGGTGCAGCAGCAGCACAATGGAATCATCTTCCAGTTTG 4056
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Db    841 TGATCAATTTGGGCTTGGTTTACAAGGTGCAGCAGCAGCACAATGGAATCATCTTCCAGTTTG 900

Qy   4057 TGGCTTTCATCAAACGAAGGCAAAGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGAT 4116
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Db    901 TGGCTTTCATCAAACGAAGGCAAAGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGAT 960

Qy   4117 ATGACCTGCTAATTCCCCAGTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCA 4176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGACCTGCTGATTCCCCAGTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCA 1020

Qy   4177 TTGGGGTCAGCATAGCTATAGACAAGATATCTGCTGCTGTCCTCAACATGGAGAATCTG 4236
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Db   1021 TTGGGGTCAGCATAGCTATAGACAAGATATCTGCTGCTGTCCTCAACATGGAGAAATCTG 1080

Qy   4237 TTACAATAAGCTCTTGTGACCTCCTGGTTGTAAGTGTTGGTCAGATGTCTATGTCCAGGG 4296
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Db   1081 TTACAATAAGCTCTTGTGACCTCCTGGTTGTAAGTGTTGGTCAGATGTCTATGTCCAGGG 1140

Qy   4297 CCATCAACCTAACCCAGAAACTCTGGACAGCAGGCATCAACGAGTACTGCAGAAATCATGTACGACT 4356
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Db   1141 CCATCAACCTAACCCAGAAACTCTGGACAGCAGGCATCAACGAGTACTGCAGAAATCATGTACGACT 1200

Qy   4357 GGTCACAGTCCCAAGAGAATTACAAGAGTACTGCAGCATCATGAAATCACCTATGTGG 4416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGTCACAGTCCCAAGAGAATTACAAGAGTACTGCAGCATCATGAAATCACCTATGTGG 1260

Qy   4417 CCCTTGTCTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTCGAGAAGGAAAGGC 4476
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Db   1261 CCCTTGTCTCGGATAAAGAAGGAAGCCATGTCAAGGTAAAGTCTTTCGAGAAGGAAAGGC 1320

Qy   4477 AGACAGAGAAGCGTGTGTCGGAGACTGAACTTGTGGACCATGTAACTGTACTGCAGAAAACTGAGGA 4536
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Db   1321 AGACAGAGAAGCGTGTGTCGGAGACTGAACTTGTGGACCATGTAACTGTACTGCAGAAAACTGAGGA 1380

Qy   4537 CTAAAGTCACTGATGAAAGCGAATGGCAGAGAAGCTTCCGATAATCTTGCAGTGCAAAATC 4596
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Db   1381 CTAAAGTCACTGATGAAAGGCAGAGAAGCTTCCGATAATCTTGCAGTGCAAAATC 1440

Qy   4597 TGAAGGGGTCATTTCTAATGCTTCAGGTTGTCAGGGTTTGTTGAAATCCATGGAGCACAGTCGTTC 4656
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Db   1441 TGAAGGGGTCATTTCTAATGCTTCAGGTTTGTTGAAATCCATGGAGCACAGTCGTTC 1500

Qy   4657 CCATTGTGAGTGTGCTAGCCCCGGAGAGCTGTCAGCCAGCACTAGGAGGGCTATGAAA 4716
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Db   1501 CCATTGTGAGTGTGCTAGCCCCGGAGAGCTGTCAGCCAGCACTAGGAGGGCTATGAAA 1560

Qy   4717 CTCAGGTACAAAACTCGACTTCAGACCTCCCTTGCCAACTTACCACTACAGAAAGCAGTGAAA 4776
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Db   1561 CTC--------------------------------------------------------- 1563

Qy   4777 TTGAAATTCTGGCTGTGGGATCTACCCCAAAGAAACAATATTACAGTTTTTATCATTAGAGT 4836
          ----------------------------------------------------------AGT 1566

Qy   4837 GGGATGCTGATGAACACAGGCATTAACACAACGTGCTGTCACGGCTCGCCGCCAA 4896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 GGGATGCTGATGAACACAGGCATTAACACAACGTGCTGTCACGGCTCGCCGCCAA 1626

Qy   4897 AGCAAAGATACCCCAAATTAGTCTGTGATGAAATTTATAAACATCAAAGTAGAAAAAAGG 4956
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 AGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAAACATCAAAGTAGAAAAAAAGG 1686

Qy   4957 TGTCTGTGCTATTTCTGTACAGTTGCACTATAGAGATGACTACCTACAGAATCTTATTTTAACCCT 5016
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 TGTCTGTGCTATTTCTGTACAGTTGCACTATAGAGATGACTACCTACAGAATCTTATTTTAACCCT 1746

Qy   5017 AAAGAACTGTCGTTAACCTCATTCAAACAGACAGAGAGGCTTATACTGGAATAATGGAATGT 5076
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 AAAGAACTGTCGTTAACCTCATTCAAACAGACAGAGAGGCTTATACTGGAATAATGGAATGT 1806
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Qy   5077  TGTACATTCATCATAATTAAAATTAAAATTCTAAGAAGA  5115
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Db   1807  TGTACATTCATCATAATTAAAATTAAAATTCTAAGAAGA  1845
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RESULT 12
US-10-204-887-29
; Sequence 29, Application US/10204887
; Publication No. US20030124569A1
GENERAL INFORMATION:
;   APPLICANT: INCYTE GENOMICS, INC.
;   APPLICANT: PANZER, Scott R.
;   APPLICANT: SPIRO, Peter A.
;   APPLICANT: BANVILLE, Steven C.
;   APPLICANT: SHAH, Purvi
;   APPLICANT: CHALUP, Michael S.
;   APPLICANT: CHANG, Simon C.
;   APPLICANT: CHEN, Alice
;   APPLICANT: D'SA, Steven A.
;   APPLICANT: AMSHEY, Stefan
;   APPLICANT: DAHL, Christopher R.
;   APPLICANT: DAM, Tam C.
;   APPLICANT: DANIELS, Susan E.
;   APPLICANT: DUFOUR, Gerard E.
;   APPLICANT: FLORES, Vincent
;   APPLICANT: FONG, Willy T.
;   APPLICANT: GREENAWALT, Lila B.
;   APPLICANT: HILLMAN, Jennifer L.
;   APPLICANT: JONES, Anissa L.
;   APPLICANT: LIU, Tommy F.
;   APPLICANT: ROSEBERRY, Ann M.
;   APPLICANT: ROSEN, Bruce H.
;   APPLICANT: RUSSO, Frank D.
;   APPLICANT: STOCKDREHER, Theresa K.
;   APPLICANT: DAFFO, Abel
;   APPLICANT: WRIGHT, Rachel J.
;   APPLICANT: YAP, Pierre E.
;   APPLICANT: YU, Jimmy Y.
;   APPLICANT: BRADLEY, Diana L.
;   APPLICANT: BRATCHER, Shawn R.
;   APPLICANT: CHEN, Wensheng
;   APPLICANT: COHEN, Howard J.
;   APPLICANT: HODGSON, David M.
;   APPLICANT: LINCOLN, Stephen E.
; NUMBER OF SEQ ID NOS: 159
; TITLE OF INVENTION: SECRETORY MOLECULES
; FILE REFERENCE: PT-1134 PCT
; CURRENT APPLICATION NUMBER: US/10/204,887
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/185,215; 60/185,216; 60/205,323; 60/205,287;
    60/205,324; 60/205,286
; PRIOR FILING DATE: 2000-02-24; 2000-02-24; 2000-05-16; 2000-05-17; 2000-05-17;
    2000-05-17; 2000-05-17
; SOFTWARE: PERL Program
; SEQ ID NO 29
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: misc feature
;   OTHER INFORMATION: Incyte ID No. US20030124569A1 LI:213087.1.:2000MAY01
; FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 592, 601
;   OTHER INFORMATION: a, t, c, g, or other
US-10-204-887-29

Query Match   16.1%;   Score 886.8;   DB 14;   Length 897;
Best Local Similarity 99.6%;   Pred. No. 7.3e-230;
Matches 888;   Conservative   0;   Mismatches   4;   Indels   0;   Gaps   0;

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Qy    49  GGCGCAGCGCGCTGCCATGGCGTGGGGCCGTGGGGCCCCGGGGGCGGGGGGACGAGCCTC  108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6  GGGCAGCCGCTGCCATGGCGTGGGGCCGTGGGGCCCCGGGGGCGGGGGGACGAGCCTC    65

Qy   109  CGGAGAGCTACCCGCCAACGACCAGCAGGACCGACGACTACAGGCCGCTGGGAGAGGCCCATCTACGGCG  168
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    66  CGGAGAGCTACCCGCCAACGACCAGCAGGACCGACGACTACAGGCCCTGGGAGGGCCCATCTACGGCG    125

Qy   169  CGGACTTCCAAGACCTGGGCCCGACGCTTGCGGACCGGTCAAAGAGACCCCCTGAAATCA  228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126  CGGACTTCCAAGACCTGGGCCCGACGCTTGCGGACCGGTCAAAGAGACCCCCTGAAATCA  185

Qy   229  ATTTAGTTTGTACCCTCAAGGCTAACTGGTGAAGAAGTATATGTAAAAGTGGATTTGA   288
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186  ATTTAGTTTGTACCCTCAAGGCTAACTGGTGAAGAAGTATATGTAAAAGTGGATTTGA   245

Qy   289  GGGTAAATGCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGACTTAAAAAATGCCA  348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246  GGGTAAATGCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGACTTAAAAAATGCCA  305

Qy   349  AAGGTCTATCAAATGAAAGTGTCAATTTGTAAAATCTCGGCCTAGAAGAACTGGCCAAGA  408
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306  AAGGTCTATCAAATGAAAGTGTCAATTTGTTAAAATCTCGGCCCTAGAAGAACTGGCCAAGA  365

Qy   409  AACACTGTGGGAGGTGATGATCTTGAACTGGCTTACCACGTGCGAGTCATTCTCAGCG   468
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366  AACACTGTGGGAGGTGATGATCTTGAACTGGCTTACCACGTGCGAGTCATTCTCAGCG   425

Qy   469  AGCATAACAAGCCCCCTCCCAAGTCTTTCATGAAGAAATGCTGGAAAGGCGGGCTCAGG  528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426  AGCATAACAAGCCCCCTCCCAAGTCTTTCATGAAGAAATGCTGGAAAGGCGGGCTCAGG  485

Qy   529  AGGAGCAGCAGAGGCTGTTGGAGCCAAGCGAAAGAAAGAGCAGGAGCAACGTGAAATCC  588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486  AGGAGCAGCAGAGGCTGTTGGAGCCAAGCGAAAGAAAGAGCAGGAGCAACGTGAAATCC  545

Qy   589  TGCATGAGATTCAGAGAGGAAAGAAGAAGATAAAAAGGAAAGAAAGANATGG         648
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   546  TGCATGAGATTCAGAGAGGAAAGAAGAAGATAAAAAGGAAAGAAAGANNATGG        605

Qy   649  CTAAGCAGGAACGTTTGGAAATTGCTAGTTTGTCAAACCAAGATCATACCTCTAAGAAGG  708
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606  CTAAGCAGGAACGTTTGGAAATTGCTAGTTTGTCAAACCAAGATCATACCTCTAAGAAGG  665

Qy   709  ACCCAGGAGGACACAGAACGGCTGCCATTCACATGGAGGCTCTCCTGACTTTGTAGGAA  768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666  ACCCAGGAGGACACAGAACGGCTGCCATTCACATGGAGGCTCTCCTGACTTTGTAGGAA  725

Qy   769  ATGGTAAACATCGGCAAACTCCTCAGGAAGGTCTAGGCGAGACGTCAGTATTCTGTAT   828
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726  ATGGTAAACATCGGCAAACTCCTCAGGAAGGTCTAGGCGAGACGTCAGTATTCTGTAT   785

Qy   829  GTAATAGTGAAGATTCTCCTGGCTCTTGTATTTCAATATGGGAGTCCTG           888
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   786  GTAATAGTGAAGATTCTCCTGGCTCTTGTATTTCAATATGGGAGTCCTG           845

Qy   889  ATCAGCTCATGGTGCACAAAGGAAAATGTATTGGCAGTGATGAACAACTGG         940
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Db   846  ATCAGCTCATGGCGCCCAAAGGAAAATGTATTGGCAGTGATGAACAACTGG         897
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RESULT 13
US-09-998-598-753
; Sequence 753, Application US/09998598
; Patent No. US20020150922A1
GENERAL INFORMATION:
;   APPLICANT: Stolk, John A.
;   APPLICANT: Xu, Jiangchun
;   APPLICANT: Chenault, Ruth A.
;   APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598

CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 753
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-753

Query Match 9.4%; Score 517.4; DB 9; Length 519;
Best Local Similarity 99.8%; Pred. No. 1.4e-129;
Matches 518; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 3464 AAAACGATACTGCATAGAACGTGTGTTCAGGCCGCGCAAGTTAGATCGATTTCATCCCAA 3523
Db    1 AAAACGATACTGCATAGAACGTGTGTTCAGGCCGCGCAAGTTAGATCGATTTCATCCCAA   60

Qy 3524 AGAACTTCTGGAGTGTGCATTGATATGTCACTTCTACCACCAACAGCTTTCTTCTGCCCAC 3583
Db   61 AGAACTTCTGGAGTGTGCATTGATATGTCACTTCTACCACCAACAGCTTTCTTCTGCCCAC  120

Qy 3584 TGCTGAAATTATCACTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAG 3643
Db  121 TGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAG  180

Qy 3644 AAATTACAGTATTATTTGAACCATACCATGTTATTGAAAGCAATACTCTTACACTGTGG 3703
Db  181 AAATTACAGTATTATTTGAACCATACCATGTTATTGAAAGCAATACTCTTACACTGTGG  240

Qy 3704 GATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGACAGAGAA 3763
Db  241 GATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGACAGAGAA  300

Qy 3764 GCTGACGAGGAGGAGAAGTGAAGCTAAATTTGTAATCTGTCTTTGTCTTCTTAATAGTCT 3823
Db  301 GCTGACGAGGAGGAGAAGTGAAGCTAAATTTGTAATCTGTCTTTGTCTTCTTAATAGTCT  360

Qy 3824 GTGTCGACTCTACAAGTTTATTGAACACAGAAGGGAGATTTGCAAGATCTTATGCCAACAAT 3883
Db  361 GTGTCGACTCTACAAGTTTATTGAACACAGAAGGGAGATTTGCAAGATCTTATGCCAACAAT  420

Qy 3884 AAATTCATTAATAAACACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGA 3943
Db  421 AAATTCATTAATAAACACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGA  480

Qy 3944 CCTAGAGGAGGTTGTTGGACTGTTGAAGAAACTCGGCAT 3982
Db  481 CCTAGAGGAGGTTGTTGGACTGTTGAAGAAACTCTGCAT  519
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RESULT 14
US-10-006-285-340
; Sequence 340, Application US/10006285
; Publication No. US20030165854A1
; GENERAL INFORMATION:
; APPLICANT: Mary Jane Cunningham
; APPLICANT: Matthew R. Kaser
; TITLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS
; FILE REFERENCE: PA-0039 US
; CURRENT APPLICATION NUMBER: US/10/006,285
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 514
; SOFTWARE: PERL Program
; SEQ ID NO 340
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165854A1 237271_Rn.1
US-10-006-285-340

Query Match 6.8%; Score 373.4; DB 14; Length 471;

Best Local Similarity 87.0%; Pred. No. 1.8e-90;
Matches 410; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

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Qy 4083 GCTGTACCTGAAATCCTCGCAGCTGGAGGCAGATATGACCTGCTGATTCCCAGTTTAGA 4142
Db    1 GTTGTGCCTGAGATCCTTGCGCTGCTGGCAGATATGACCTGCTGATTCCCAAGTTCAGA   60

Qy 4143 GGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCATTGGGGTCAGCATAGCTATAGACAAG 4202
Db   61 GGCCCACAGGCTCTGGGGCCAGTTCCCACTGCCAGTCGTGTCGGTGTCAGCATAGACAAG  120

Qy 4203 ATATCTGCTGCTGTCCTCAACATGGGAGGAAATCTGTTACAATAAGCTTCTTGTGACCTCCTG 4262
Db  121 ATATTCGCGCCGTCGTCCTCAACATGGGAGGAGCCGTGTTACAGTGAGCTTCCTGTGACCTCCTG  180

Qy 4263 GTTGTAAGTGTTGGTCAGATGTCTATGTCCAGGGCCATCACCAGAAACTCTGG 4322
Db  181 GTTGTCAGTGCTGCTGGCCAGATGTCCATGTCCAGGGCCATCACCAGAAACTCTGG  240

Qy 4323 ACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACAGTCCCAAGAGAGGAATTACAA 4382
Db  241 ACGGCCGGCATCACTGCAGAGATCATGTACTGGTCACAGTCCCAGGAGAGTTACAA  300

Qy 4383 GAGTACTGCAGACATCATGAATCACCTATGTGGCCCTTGTCTCGGATAAAGAAGGAAGC 4442
Db  301 GAATACTGCAGACATCACGAAATCACCTATGTGGCCCTGGTCTCTGATAAAGAAGGAAGC  360

Qy 4443 CATGTCAAGGTTAAGTCTTCGAGAAGGAAGGCAGAGAGGCAAACAGAAAACGTGTGTGGAGACT 4502
Db  361 CATGTCAAGGTCAAGTCCTTGAGAAGGAAGGGCAGAGAGGCAAACAGAAAACGTGTGTTGGAATCA  420

Qy 4503 GAACTTGTGGACCATGTACTGCGAGAAACTGAGAACTAAAGTCACTGATGAA 4553
Db  421 GATCTTGTGGACCATGTTATGCGAGAAACTAAGGACCAAAGTTGGTGACGAA  471
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RESULT 15
US-10-062-674-1525
; Sequence 1525, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1525
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 1178685.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(691)
; OTHER INFORMATION: a, t, c, g, or other
US-10-062-674-1525

Query Match 6.7%; Score 368.4; DB 15; Length 691;
Best Local Similarity 54.9%; Pred. No. 5.6e-89;
Matches 380; Conservative 0; Mismatches 311; Indels 1; Gaps 1;

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Qy 4820 GTTTTATCATTAGAGTGGGATGCTGATGAACAGGCATTTAACACAACTGTGAAGCAGCT 4879
Db    1 GTTTTTATCATTAGAGTGGGATGGCTGATGAACAGGCATTTAACACAACTGTGAAGCAGCT   60

Qy 4880 GCTGTCACGCCTGCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACAT 4939
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Db      61 GCTGTCACGCCTGCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAAACAT 120

Qy    4940 CAAAGTAGAGAAAAAAGGTGTCTGCTATTTCTGTACAGCTATAGAGATGACTACTACAG 4999
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAAAGTAGAGAAAAAAGGTGTCTGCTATTTCTGTACAGCTATAGAGATGACTACTACAG 180

Qy    5000 AATCCTATTTTAACCCTAAAGAACTGTCGTTAACCTCATTCAAACACAGACAGAGGCTTATA 5059
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AATCCTTATTTTAACCCTAAAGAACTGTCGTTAACCTCATTCAAACACAGACAGAGGCTTATA 240

Qy    5060 CTGGAATAATGGAATGTTGTACATTCATCATAATTTAAAATTAAATTCTAAGAAGAGGCT 5119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGGAATAATGGAATGTTGTACATTCATCATAATTTAAAATTAAATTCTAAGAAGA-NNN 299

Qy    5120 GGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGC 5179
Db     300 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 359

Qy    5180 TTGAAACCAGGAGTTTGAGACCAGCCTGAGCAACAAAGCAAGACCCCATCTCTATAAAAA 5239
Db     360 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 419

Qy    5240 CTAAAAAATTAGTTGGGCATGGTGGCACATGCCTGTAGTCCCAGCTACTCCAGAGGCTG 5299
Db     420 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 479

Qy    5300 AGATGGATCATCTGAGCCTCAGGAGGTTGAGGCTGCAGTGAGCTGTGACTGCGCCACTGC 5359
Db     480 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 539

Qy    5360 ACTCCAGTCTGGGACAACAGAGCAAGACCCTGTCTTAAAAAAAAGAAAAAAATTT 5419
Db     540 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 599

Qy    5420 TTTTTCTAAGAAGCTGTCCTACAAAGTTGAGCTTTGTTAGTTTTTCATGTGTAATATATT 5479
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 NNNNNNNAAGAAGCTGTCCTACAAAGTTGAGCTTTGTTAGTTTTTCATGTGTAATATATT 659

Qy    5480 ATAAATTTATCTTTTGGGATATAATAAATGCT 5511
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Db     660 ATAAATTTATCTTTTGGGGTATAATAAATGCT 691
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                Copyright   GenCore version 5.1.6
                            (c) 1993 - 2004 Compugen Ltd.

DM protein - nucleic search, using frame_plus_p2n model

Run on:     March 21, 2004, 22:14:49 ; Search time 175 Seconds
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            Ygapop 10.0 , Ygapext 0.5
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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1	480.5	5.6	2729	1	US-07-938-782A-1	Sequence 1, Appl
2	480.5	5.6	2729	1	US-08-630-524-1	Sequence 1, Appl
3	480.5	5.6	2729	5	PCT-US93-08131-1	Sequence 1, Appl
4	470	5.5	1887	4	US-09-799-875-18	Sequence 18, Appl
5	470	5.5	2870	4	US-09-799-875-16	Sequence 16, Appl
6	470	5.5	2891	4	US-09-578-441-1	Sequence 1, Appl
7	443	5.2	244	4	US-09-016-434-785	Sequence 785, App
8	416	4.9	2628	1	US-08-143-219-1	Sequence 1, Appl
9	413.5	4.8	2562	2	US-08-436-771-8	Sequence 8, Appl
10	413.5	4.8	2562	2	US-08-434-998-8	Sequence 8, Appl
11	413.5	4.8	2562	2	US-08-487-797-8	Sequence 8, Appl
12	413.5	4.8	2562	5	PCT-US95-02058-8	Sequence 8, Appl
13	358	4.2	2827	4	US-09-554-726A-11	Sequence 11, Appl
14	358	4.2	2827	4	US-09-554-726A-20	Sequence 20, Appl
15	321	3.8	4307	4	US-09-803-671B-1	Sequence 1, Appl
16	317.5	3.7	2157	4	US-09-371-338-16	Sequence 16, Appl
17	317	3.7	2527	4	US-09-371-338-20	Sequence 20, Appl
18	305.5	3.6	2076	4	US-09-554-726A-1	Sequence 1, Appl
19	305	3.6	2155	4	US-09-371-338-8	Sequence 8, Appl
c 20	303.5	3.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 21	303.5	3.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
22	302.5	3.5	802	4	US-09-371-338-10	Sequence 10, Appl
23	300	3.5	2193	4	US-09-371-338-12	Sequence 12, Appl
24	296.5	3.5	804	4	US-09-371-338-14	Sequence 14, Appl
25	295.5	3.5	804	4	US-09-371-338-22	Sequence 22, Appl
26	294.5	3.4	804	4	US-09-371-338-18	Sequence 18, Appl
27	292	3.4	1744	4	US-09-685-462-9	Sequence 9, Appl
28	284.5	3.3	3089	1	US-08-472-934-5	Sequence 5, Appl
29	284.5	3.3	3089	2	US-08-323-460A-5	Sequence 5, Appl
30	284.5	3.3	3089	2	US-08-461-146C-5	Sequence 5, Appl
31	284.5	3.3	3089	2	US-08-461-145C-5	Sequence 5, Appl
32	284.5	3.3	3332	4	US-08-628-828-9	Sequence 9, Appl
33	284	3.3	1542	4	US-09-423-890-11	Sequence 13, Appl
34	283	3.3	282	3	US-09-345-473A-13	Sequence 13, Appl
35	282	3.3	3201	2	US-09-211-930-1	Sequence 1, Appl
36	282	3.3	3201	3	US-09-346-993-1	Sequence 1, Appl
37	282	3.3	3201	4	US-09-468-442-1	Sequence 1, Appl
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42	277	3.2	5236	3	US-09-359-757-1	Sequence 13, Appl
c 43	273	3.2	7685	4	US-09-221-017B-1092	Sequence 1092, Ap
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45	270	3.2	2028	2	US-09-211-930-12	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
US-07-938-782A-1
; Sequence 1, Application US/07938782A
; Patent No. 5525513
; GENERAL INFORMATION:
;   APPLICANT: Chen, Jane J.
;   APPLICANT: London, Irving M.
;   TITLE OF INVENTION: DNA Encoding the Heme-Regulated
;   TITLE OF INVENTION: Eukaryotic Initiation Factor 2 alpha kinase
;   NUMBER OF SEQUENCES: 15
;   CORRSPONDENCE ADDRESS:
;     ADDRESSEE: Patrea L. Pabst
;     STREET: 2800 One Atlantic Center
;     STREET: 1201 West Peachtree Street
;     CITY: Atlanta
;     STATE: Georgia
;     COUNTRY: US
;     ZIP: 30309-3450
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07/938,782A
;     FILING DATE: 31-AUG-1992
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Pabst, Patrea L.
;     REGISTRATION NUMBER: 31,284
;     REFERENCE/DOCKET NUMBER: WU101CIP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (404)873-8794
;     TELEFAX: (404)873-8795
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
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LENGTH: 2729 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rabbit
CELL TYPE: Reticulocytes
FEATURE:
NAME/KEY: misc_feature
LOCATION: 113..2149
OTHER INFORMATION: /note= "Expression of HRI
OTHER INFORMATION: mRNA in Human erythroid cells, using as the
OTHER INFORMATION: probe rabbit HRI cDNA from nucleotides 113
OTHER INFORMATION: to 2149."
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NAME/KEY: misc_feature
LOCATION: 229..249
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OTHER INFORMATION: amplification of human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
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OTHER INFORMATION: using the rabbit HRI cDNA sequence."
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OTHER INFORMATION: using the rabbit HRI cDNA sequence."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1009..1031
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OTHER INFORMATION: amplification of a human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
PUBLICATION INFORMATION:
AUTHORS: Chen, Jane J.
AUTHORS: London, Irving M.
TITLE: Cloning of the cDNA of the heme-
TITLE: regulated eukaryotic initiation factor
TITLE: 2alpha (eIF-2alpha)kinase of rabbit reticulocytes:
TITLE: Homology to yeast GCN2 protein kinase and human
TITLE: double-stranded-RNA-dependent
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 88
PAGES: 7729-7733
DATE: September-1991

US-07-938-782A-1

Alignment Scores:
Pred. No.:   1.33e-38
Score: 480.50
Percent Similarity: 43.91%
Best Local Similarity: 28.75%
Query Match: 5.62%
DB: 1

Length: 2729
Matches: 184
Conservative: 97
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Gaps: 29

US-09-515-806A-2 (1-1649) x US-07-938-782A-1 (1-2729)

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; Sequence 1, Application US/08630524
; Patent No. 5690930
GENERAL INFORMATION:
   APPLICANT: Chen, Jane J.
   APPLICANT: London, Irving M.
   TITLE OF INVENTION: DNA Encoding the Heme-Regulated
   TITLE OF INVENTION: Eurkaryotic Initiation Factor 2 alpha kinase
   NUMBER OF SEQUENCES: 15
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Patrea L. Pabst
   STREET: 2800 One Atlantic Center
   STREET: 1201 West Peachtree Street
   CITY: Atlanta
   STATE: Georgia
   COUNTRY: US
   ZIP: 30309-3450
   COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/08/630,524

FILING DATE: 10-APR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US 07/938,782
   FILING DATE: 31-AUG-1992
ATTORNEY/AGENT INFORMATION:
   NAME: Pabst, Patrea L.
   REGISTRATION NUMBER: 31,284
   REFERENCE/DOCKET NUMBER: WU101CIP
TELECOMMUNICATION INFORMATION:
   TELEPHONE: (404)873-8794
   TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 1:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 2729 base pairs
   TYPE: nucleic acid
   STRANDEDNESS: single
   TOPOLOGY: linear
   MOLECULE TYPE: cDNA
   HYPOTHETICAL: NO
   ANTI-SENSE: NO
   FRAGMENT TYPE: N-terminal
   ORIGINAL SOURCE:
   ORGANISM: Rabbit
   CELL TYPE: Reticulocytes
FEATURE:
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   LOCATION: 113..2149
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   OTHER INFORMATION: mRNA in Human erythroid cells, using as the
   OTHER INFORMATION: probe rabbit HRI cDNA from nucleotides 113
   OTHER INFORMATION: to 2149."
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   OTHER INFORMATION: /note= "Primer used in the
   OTHER INFORMATION: amplification of human HRI cDNA sequence
   OTHER INFORMATION: using the rabbit HRI cDNA sequence."
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   OTHER INFORMATION: using the rabbit HRI cDNA sequence."
PUBLICATION INFORMATION:
   AUTHORS: Chen, Jane J.
   AUTHORS: London, Irving M.
   TITLE: Cloning of the cDNA of the heme-
   TITLE: regulated eukaryotic initiation factor
   TITLE: 2alpha (eIF-2alpha)kinase of rabbit reticulocytes:
   TITLE: Homology to yeast GCN2 protein kinase and human
   TITLE: double-stranded-RNA-dependent
   JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
   VOLUME: 88
   PAGES: 7729-7733
   DATE: September-1991

US-08-630-524-1

Alignment Scores:
Pred. No.:   Length: 2729
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Qy  816 GlnGlyLeu------TyrArgAspThrValArgLeuTrpArgLeuPheArgGlyIleLeuLeu 833
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Qy  854 IlePheLeuAspSer--AspAspHisValLysIleGlyTyrAspPheGlyLeuAlaThrAsp 872
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Db 2290 ATCCTGGCCACCTGCTCCTTTAGAAGCACACTCACTCGCCCCGCCACCACCCAAGG 2345
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CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08131
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT 5807
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2729 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rabbit
CELL TYPE: Reticulocytes
FEATURE:
NAME/KEY: misc_feature
LOCATION: 113..2149
OTHER INFORMATION: /note= "Expression of HRI mRNA in Human erythroid cells,
FEATURE:
NAME/KEY: misc_feature
LOCATION: 229..249
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NAME/KEY: misc_feature
LOCATION: 543..560
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NAME/KEY: misc_feature
LOCATION: 448..468
OTHER INFORMATION: /note= "Primer used in the amplification of human HRI cDN
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1009..1031
OTHER INFORMATION: /note= "Primer used in the amplification of a human HRI c
PUBLICATION INFORMATION:
AUTHORS: London, Irving M.
Chen, Jane J.
TITLE: Cloning of the cDNA of the heme-regulated
TITLE: eukaryotic initiation factor 2alpha
TITLE: (eIF-2alpha)kinase of rabbit reticulocytes:
TITLE: Homology to yeast GCN2 protein kinase and human
TITLE: double-stranded-RNA-dependent
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 88
PAGES: 7729-7733
DATE: September-1991
PCT-US93-08131-1
```

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Alignment Scores:
Pred. No.:            1.33e-38
Score:                480.50
Percent Similarity:   43.91%
Best Local Similarity: 28.75%
Query Match:          5.62%
Length:               2729
Matches:              184
Conservative:         97
Mismatches:           241
Indels:               119
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US-09-515-806A-2 (1-1649) x PCT-US93-08131-1 (1-2729)

Qy  580  GlnArgGlnPheSerArgTyrPheIleGluPheGluGlnLeuGlnLeuLeuGlyLeuGlyLysGly  599
              ::|||   ||||            ::::::   |||||  |||||
Db  590  GAAGCAGACCTCACGATACTTGAATGAGTTTGAAGAGCTCTCCATCCTGGGGAAAGGT  649

Qy  600  AlaPheGlyAlaValIleLeuLysValGlnAsnLysLeuAspGlyCysCysTyrAlaValLys  619
              ::|||:||::|| ||||            :||| ::::::
Db  650  GGCTATGGCCGAGTGTACAAGGTCAGGAATAAATAAATTAGATGGCCAGTATTATGCAATTAAA  709

Qy  620  ArgIleProIleAsnProAlaSerArg---GlnPheArgArgIleLysGlyGluValThr  638
              ::|||            :::::::
Db  710  AAAATTCTGATTAAAGGTGCAACTAAAAACAGATTGCATGAAGGTATTACGAAGAAGTGAAA  769

Qy  639  LeuLeuSerArgLeuHisHisGluAsnIleValArgTyrTyrAsnAlaTrpIleGluArg  658
              :::|||:|| :::: |||||            |||
Db  770  GTGCTGGCGGGGCCTCCAGCACCCTAATATCGTAGGCTATCACACCGCGTGATAGAGCAT  829

Qy  659  ---HisGluArgProAlaGlyProGlyThrPro-----ProProAspSerGlyProLeu  675
              ||| |||            |||
Db  830  GTCCACGTTCACGTTCAAGCAGCAGCAGAGTTCCGATTCCAGTTGCCTTCTCTGGAAGTGCTC  889

Qy  676  Ala------LysAspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeu  693
              :::            :::::::|||
Db  890  TCTGACCAGGAAGAAGACAGAGATCAATATGGTGTTAAAAATGATGCAAGCAGCAGCTCA  949

Qy  694  AspSerValGluAlaIleAlaProProProIleLeuSerSerValGluTrpSerThr  713
              ||| |||            :::    :::
Db  950  TCCATTATTTTCGGTGAGTTCTCCCAGAAAAAGAAAAATCCTCTGACGAATGTGCCCGTT  1009

Qy  714  SerGlyGluArgSerAlaSerAlaAsrgPheProAla----------ThrGly  727
              ::: :::                                   |||
Db  1010 GAGAGTCAGAATAACAAACTGGTGAACTACCACCACCACCACTTAGTGGTGAGGGACACCGGT  1069

Qy  728  ProGlySerSerAspAspGluAspAspGluGluHisGlyGlyValPheSerGln  747
              |||   ::|||            :::
Db  1070 GAGTTTGAATCGTCCACGGAG------CGCCAAGAGAACGGCTCGATCGTGAGCGT  1120

Qy  748  SerPheLeuProAlaSerAspSerGluSerAspIleIlePheAspAsnGluAspAsn  767
              :::::            :::   |||
Db  1121 CAGCTACTGTTCGGGCATAACTCAGACCTAGAA------GAGGATTTCACG  1165

Qy  768  SerLysSerGlnAsnGlnAspCysAsnGluLysAsnGlyCysHisGluSerGlu  787
              ::::::            :::
Db  1166 TCCGCGGAGGAAATCTTCTGAGGAAGACTTAAGCGCGTTGCGG------  1207

Qy  788  ProSerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCys  805
              :::::                       |||:::|||:::
Db  1208 --------CACACAGAGTGCAGTACCACCTGCATATCCAGATGCAGCTCGTGC  1258

Qy  806  GluLysSer------------------ThrLeuArgAspThrIleAspAsp  815
              |||||                    :::
Db  1259 GAGCTGTCCCTGTCCCTGTGGACTGGATCGCCGGAGAGAACAGGCGGAGTGCGTGGAC  1318

Qy  816  GlnGlyLeu------TyrArgAspThrValArgLeuTyrArgLeuPheArgGluIleLeu  833
              :::            |||
Db  1319 GAATCTGCCTGTCCTTATGTTATGGTCAGTGTGCAACAAAATTTTCAGAACTGGTG  1378

Qy  834  AspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsn  853
              ::|||            |||:::|||
Db  1379 GAAGGTGTGTTTACATACATAACATGGCATCGTGACAGAGACCTGAAGCCTAGAAAT  1438

Qy  854  IlePheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAlaThrAsp  872
              :::            :::
Db  1439 ATTTTTCTTCATGGTCCTGATCAACAAGTGAAAATAGGAGACTTTGGTCTGGCC------  1492

Qy  873  HisLeuAlaPheSerAlaAspSerLysLysAspAspGlnThrGlyAspLeuIleLysSer  892
              |||            :::
Db  1493 ------------TGCGCCGACATCATCAGAAGAAATGCGGCCCGGACCAGCAGAAAACGGG  1540

Qy  893  AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu---  911
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; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 18
;   LENGTH: 1887
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-799-875-18

Alignment Scores:
Pred. No.:                                    Length:            1887
Score:              8.16e-38                  Matches:            161
Percent Similarity: 470.00                    Conservative:        69
Best Local Similarity: 47.03%                 Mismatches:         185
Query Match:        32.92%                    Indels:              74
DB:                  5.50%                     Gaps:                22
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US-09-515-806A-2 (1-1649)  x  US-09-799-875-18 (1-1887)

Qy   550  GlnSerProGluSerGlyGlyGlnAspTyrValGluThrValIleProSerAsnArg 569
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Db   445  ATCAGATCAAGGGAAGGAAGTAGCCTGGAAGCACAAACT-----TCACGTTACTAAATGAA 498

Qy   590  PheGluGluLeuGlnLeuLeuGlyLysGlyAlaPheGlyAlaValIleLysValGlnAsn 609
          ||:||                                          |||
Db   499  TTTGAAGAACTTGCCATCTTAGGAAAAGGTGGATACCGAAGAGTATACAAGGTCAGGAAT 558

Qy   610  LysLeuAspGlyCysCysTyrAlaValLysValLysArgIleProIleAsnProAlaSerArgGln 629
          :::|||                                          ||||:|||
Db   559  AAATTAGATGGTCAGTATTATGCAATAAAAAAATCCTGATTAAGGGTGCAACTAAAACA 618

Qy   630  Phe--ArgArgIleLysGlyGluValThrLeuSerArgLeuHisSerGluAsnIle 648
          :: :                                       ||:|||
Db   619  GTTTGCATGAAGGTCCTACGGAAGTGAAGGTGCTGCAGGTCTTCAGCACCCCATATT 678

Qy   649  ValArgTyrTyrAsnAlaTrpIleGluArgHisGluArgGlyProAlaGlyProGlyThrPro 668
          ||||                                       |||
Db   679  GTTGGCTATCACACCGCGTGAATAGAA---CATGTTCATGTGATTCAGCCA----------- 726

Qy   669  ProProAspSerGlyProLeuAlaLysAspArgArgAlaAlaLysArgGlyGlnProAla-- 687
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Db   727  -----------------------------CGAGACAGAGCTGCCATTGAGTGCCATCCTG 759

Qy   688  -----------------------------------------------SerAspThrAsp 691
                                                          :::|||
Db   760  GAAGTGCTCCGACCAGGAGGAGCAGAGAGCAATGTGGTGTTAAAATGATGAAAGT 819

Qy   692  GlyLeuAspSerValGluAlaAlaAlaProProLeuSerSerSerVal--Glu 710
          ::|||                                          |||
Db   820  AGCAGCTCATCCATTATCTTTGCTGAGCCCAGAAAAAGAAAACGCTTTGGAGAA 879

Qy   711  TrpSerThrSerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro 728
          ::: ||||                                         :::||||
Db   880  TCTGACACTGAAAATCAGAATAACAAGTCGGTGAAGTACACCACCAATTAGTCATAAGA 939

Qy   729  GlySerSerAspAspGluAspGluHisGlyGlyValPheSerGlnSer 748
          ::: ||||                                   :::||||
Db   940  GAATCTGGTGAACTTGATCGACCCTGAGTCTCCAGGAAAAATGGCTTGGCTGGTTTGTCT 999

Qy   749  PheLeuProAlaSerAspSerGluSerAspIleIlePheAspAsnGluAsnSer 768
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Db  1000  ------GCCAGTTCAATTGTGAACAGCAGCTGCCACTCAGGCGTAATTCCACCTAGAG 1053

Qy   769  LysSerGlnAsnGlnAspCysAspCysAsnGluLysGluGlyLysCysHisGluSerGluPro 788
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Db  1054  GAGAGTTTCATCCACCGAAGAATCTTCCGAAGAAAAATGTCAACTTTTTGGGTCAG--- 1110
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Db   1541  GAGAGAGCACCCACACACTTCCCAGTGGCACCTGTCTGTACGCCTGCCCGAGCAG 1600
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Qy    912  ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931
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Db   1601  TTGGAAGGA-------TCGGAGTATGATGCAAGCAGACATTACAGCGTCGGCGTG 1651
Qy    932  IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951
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Db   1652  ATCCTGCTGGAGCTC---TTCCAGCGCCTTGGGACAGAGATGAGCGGGACGAGGTCCTG 1708
Qy    952  AsnGlnLeuArg------------------AspProThrSerProLysPhePheProGluAspPhe 966
                :::|||                              |||
Db   1709  ACGGGCGTTGCGAGCTGGCCGCATACCCGACTCCCTCAGTAAGAGGTGCCCG---------- 1759
Qy    967  AspAspGlyGluHisAlaLysGlyIleHisSerValIleSerTrpLeuAsnHisAspPro 986
                |||                                       ::: |||
Db   1760  ---------------------GCGCAGGCCAAGTACGTCCAGCTGCTGACCAGGAGGAACGCG 1801
Qy    987  AlaLysArgProThrAlaThrGluLeuLeuLysSerGluLeuLeuProProPro------ 1004
                :::::::|||||                          :::|||||
Db   1802  TCCCAGCCGGCCGTCCGCCCTTCCAGCTGCTGCAGAGTGAGCTGTTCCAGAACTCCGGCAT 1861
Qy   1005  --------------------GluGluSerGluLeuHisGluValVal Leu 1015
                :::|||||                                |||:::
Db   1862  GTTAACCTCACCCTACACGATGAAGATAATAGAGAGAAAGAGAAATGAGGAACTCAAG 1921
Qy   1016  HisHisThrLeuThrAsnValAspGlyLysLysAspGlyGluGlyThrMetMetAlaGlnIlePhe 1035
                |||                                       :::|||
Db   1922  AAGCAGCTGAGCCTCCTCCCCAGGCCCGAGGGGTGAGGAGTGA-CAGGCG---------- 1971
Qy   1036  SerGlnArgIleSerProAlaIleAspTyrThrTyrAspSerArgAspIleLeuLysGlyGlyAsn 1055
                :::    |||:: :|||                       :::
Db   1972  --AGACGGAGAGGTCCCTGCCTAGCCGTCACTCGGCCACGTCAC------AGGGGAACCG 2022
Qy   1056  PheSerIleArgThrAlaLysMetGlnGlnHisValCysGluThrIleIleArgIlePhe 1075
                :::                                       |||:::---TTC
Db   2023  TGGACTTGCACTTCGCAGCAGTCAACTGGAATGGACAATTTCAAGCCTTCGAGG---TTC 2079
Qy   1076  LysArgHisGlyAlaValAlaValGlnLeuCysThrProLeuLeuLeuLeuProArgAsnArgGlnIle 1095
                |||||||                                   :::
Db   2080  AGGGCGGCATAAT------------------CCTCACTTGGAATCACTC 2109
Qy   1096  TyrGluHisAsnGluAlaAlaLeuPheMet------------------AspHisSerGlyMetLeu 1111
                ||||                                     :::||||
Db   2110  AGCCCGCCATGACTCTCCCCTCATGTCGTCTTCCGGAGGTACCTGGTGACCTCCTG 2169
Qy   1112  Val-MetLeuProPheAspLeuArgIle--ProPhe------------------ 1122
                |||||                                   :::
Db   2170  GTGACTGCTCCCAATTAAACTTACGCTTTTCCCTTTCCTATTCCGCAAGTCCCATCCTG 2229
Qy   1123  -AlaArgTyrValAlaArgAsnAsnIleLeu-----AsnLeuLysArgTyrCysIleGl 1140
                :::||||                                   :: |||
Db   2230  AGCCTCCTACCTAAGCATTAACTAACTAAATCTTAGGTATCGGTCTCCATTCTTCTCCTTGA 2289
Qy   1140  u--------ArgValPheArg-ProArgLysLeuAspArgPheHisProLys 1154
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Db   2290  ATCCTGGCCACCTGCTCCTTTAGAAGCACACTCACTCGCCCGCCACCCCAAGG 2345
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US-09-799-875-18
; Sequence 18, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 663872iel Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
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;    LOCATION: (114)...(2000)
US-09-799-875-16

Alignment Scores:
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Score:                      470.00          Matches:          161
Percent Similarity:         47.03%          Conservative:     69
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Query Match:                5.50%           Indels:           74
DB:                         4               Gaps:             22

US-09-515-806A-2 (1-1649) x US-09-799-875-16 (1-2870)

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Qy   570  LeuProSerAlaAlaPheSerGluThrGlnArgGlnPheSerArgTyrPheIleGlu      589
                                                        |||
Db   558  ATCAGATCAAGGGAAGTAGCCTTGGAAGCACAAACT-----TCACGTTACTTAAATGAA   611

Qy   590  PheGluGluLeuGlnLeuLeuGlyLysGlyAlaPheGlyAlaValIleLeuLysValGlnAsn  609
          |||||||                 :::|||       :::|||
Db   612  TTTGAAGAACTTGCCATCTTAGGAAAAGGTGATACCAAGAGTATACAAGGTCAGGAAT  671

Qy   610  LysLeuAspGlyCysCysTyrAlaValAlaValLysArgIleProIleAsnProAlaSerArgGln  629
          |||||:::            :::|||
Db   672  AAATTAGATGGTCAGTATTATGCAATAAAAAAAATCCTGATTAAGGGTCAACTAAAACA  731

Qy   630  Phe---ArgArgIleLysGlyLeuValThrLeuLeuSerArgLeuHisHisGluAsnIle  648
              :::            :::|||:::||||||
Db   732  GTTTGCATGAAGGTCCTACGGAAGTGAAGGTGCTGGCAGGTCTTCAGCACCCCAATATT  791

Qy   649  ValArgTyrTyrAsnAlaTrpIleGluArgHisGluArgProAlaGlyProGlyThrPro  668
              |||            :::
Db   792  GTTTGGCTATCACACGCGTGGATAGAA---CATGTTCATGTGATTCAGCCA---      839

Qy   669  ProProAspSerGlyProLeuAlaLysAspArgArgAlaAlaArgGlyGlnProAla---  687
                                    |||:::|||
Db   840  -------------------------CGAGACAGAGCTGCCATTGAGTTGCCATCCTG  872

Qy   688  SerAspThrAsp  691
                        :::|||
Db   873  GAAGTGCTCCGACCCAGGAAGAGGACAGAGCAATGTGGTGTTAAAAATGATGAAAGT  932

Qy   692  GlyLeuAspSerValGluAlaAlaAlaAlaProProIleLeuSerSerVal---Glu  710
          |||                 :::       :::|||:::
Db   993  TCTGACACTGAAAATCAGAATAACAAGTCGGTGAAGTACACCCAATTAGTCATAAGA  1052

Qy   711  TrpSerThrSerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro  728
               |||
Db   993  TCTGACACTGAAAATCAGAATAACAAGTCGGTGAAGTACACCCAATTAGTCATAAGA  1052

Qy   729  GlySerSerAspAspGluAspAspAspGluAspGluHisGlyLyGlyValPheSerGlnSer  748
                        :::       :::|||
Db  1053  GAATCTGGTGAACTGAGTCGACCCTGGAGCTCCAGGAAAATGGCTTGGCTGGTTTGTCT  1112

Qy   749  PheLeuProAlaSerGlyLeuSerAspIleIlePheAspAspAsnGluAspAsnSer  768
               |||            :::|||
Db  1113  ------GCCAGTTCAATTGTGGAACAGCAGCTGCCACTCAGGCGTAATTCCACCCTAGAG  1166

Qy   769  LysSerGlnAsnGlnAspGluAspGluLysAsnGluLysCysHisGluSerGluPro  788
          :::|||                 :::||||||:::
Db  1167  GAGAGTTTCACATCCACCGAGAGAATCTTCCGAGAAAATGTCAACTTTTTGGGTCAG--  1223

Qy   789  SerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCysGlu  806
          :::|||
Db  1224  ------ACAGAGGCACAGTACCACCTGATCGTGCACATCCAGAATGCAGCTGTGTGAG  1274

Qy   807  LysSerThrLeu-----------------------ArgAspThrIleAspGln  816
               |||                                :::|||:::
Db  1275  CTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAAGCGGGGCCGGGAGTATGTGGACGAG  1334
```

```
y    817  GlyLeu------TyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAsp  834
                          :::::|||||||:|:::::::||
b   1335  TCTGCCTGTCCTTATGTTATGGCCAATGTTGCCAACAAAAAATTTTCAAGAATTGGTAGAA 1394

y    835  GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle  854
                 ||:||:|:|||||||:
b   1395  GGTGTGTTTTACATACATAACATGGGAATTGTGCACCGAGATCTGAAGCCAAGAAATATT 1454

y    855  PheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAla---ThrAsp  872
               ||||||                    |||:||:|||||
b   1455  TTTCTTCATGGCCCTGATCAGCAAGTAAAAATAGGAGACTTTGGTCTGGCCTGCCACGAC 1514

y    873  HisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSer  892
                                    ||||||
b   1515  ATCCTA----------CAGAAGAACACAGACTGGACCAACAGAAACGGGAAGAGA 1559

y    893  AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--  911
               :|:|:   ||||| ::::|||
b   1560  ACACCAACA---CAT--ACGTCCAGAGTGGGTACTTGTCTGTGCGTTCACCCGGAACAG 1613

y    912  ValGlnGlySerThrLysSerThrAlaTyrAsnGlnLysValAspPheSerLeuGlyIle  931
               :||:|                 |||||||:||:
b   1614  TTGGAAGGA------TCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTG 1664

y    932  IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu  951
               :||:|       ||:
b   1665  GTCCTGCTAGAGCTC---TTTCAGCCGTTTGGAACAGAAATGGAGCGAGCAGAAGTTCTA 1721

y    952  AsnGlnLeuArgAspProThrSerProLysPheProGluProLysPheProGluAspGlyPheAspAspGlyHis  971
               ::: |||:
b   1722  ACAGGTTTAAGA------ACTGGTCAGTTGCGGAATCCCTCCGTAAA---AGGTGT 1769

y    972  AlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaArgProThr  991
               :|||||
b   1770  CCGGTGCAAGCCAAGTATATCCAGCACTTAACGAGAAGAGAAACTCATCCAGAGACCATCT 1829

y    992  AlaThrGluLeuLysSerGluLeu 1000
               ::|||||||:||||||||:|||||
b   1830  GCCATTCAGCTGCTGCAGAGTGAACTT 1856
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RESULT 6
US-09-578-441-1
. Sequence 1, Application US/09578441
. Patent No. 6562571
. GENERAL INFORMATION:
. APPLICANT: Wu, J.H. David
. APPLICANT: Omasa, Takeshi
. APPLICANT: Mantalaris, Athanassios
. APPLICANT: Tsai, Ying-Chuech
. APPLICANT: Chen, Yi-Guang
. TITLE OF INVENTION: HUMAN HEME-REGULATED INITIATION FACTOR 2 ALPHA KINASE
. FILE REFERENCE: 176/60571
. CURRENT APPLICATION NUMBER: US/09/578,441
. CURRENT FILING DATE: 2000-05-25
. PRIOR APPLICATION NUMBER: 60/135,713
. PRIOR FILING DATE: 1999-05-25
. NUMBER OF SEQ ID NOS: 5
. SOFTWARE: PatentIn Ver. 2.1
. SEQ ID NO 1
. LENGTH: 2891
. TYPE: DNA
. ORGANISM: Homo sapiens
US-09-578-441-1

Alignment Scores:
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Pred. No.:              1.79e-37     Length:        2891
Score:                  470.00       Matches:        161
Percent Similarity:     47.03%       Conservative:    69
Best Local Similarity:  32.92%       Mismatches:     185
Query Match:            5.50%        Indels:          74
                                     Gaps:            22
```

US-09-515-806A-2 (1-1649) x US-09-578-441-1 (1-2891)

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Qy    550  GlnSerProGluAspSerGlyGlyGlnAspTyrValGluThrValIleProSerAsnArg  569
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Db    466  AGGTCTGCTAAGAGAGAGTTCGTCAGGATCCTTGTGGAGGATATTTCTGTATCCAGAAA  525

Qy    570  LeuProSerAlaAlaPhePheSerGluThrGlnArgGlnPheSerArgTyrPheIleGlu  589
                  ||::|:  |||||||
Db    526  ATCAGATCAAGGGAGTAGCCTTGGAAGCACAAACT------TCACGTTACTTAAATGAA  579

Qy    590  PheGluGluLeuGlnLeuGlyLysLeuGlyAlaValIleLeuLysValGlnAsn  609
                  ||||:|:|:||:   |:::::|||::::::
Db    580  TTTGGAAGAACTTGCCCATCTTAGGAAAAAGGTGGATACGGAAGAGTATACAGGTCAGGAAT  639

Qy    610  LysLeuAspGlyCysCysTyrAlaValLysArgIleProIleAsnProAlaSerArgGln  629
                  ||||||||||||||:|:|::::::|||||:
Db    640  AAATTAGATGGTCAGTATTATGCAATAAAAAAAACCTGATTAAGGGTGCAACTAAACCA  699

Qy    630  Phe---ArgArgIleLysGlyValThrLeuLeuSerArgLeuHisHisGluAsnIle  648
                  ::::|||||::||::::|:|||
Db    700  GTTTGCATGAAGGTCCTACGGGAGGTGAAGCGGCCGCAGGTCCTTCAGCACCCCAATATT  759

Qy    649  ValArgTyrTyrAsnAlaTrpIleGluArgHisGluArgProAlaGlyProGlyThrPro  668
                  |:|||::|||::|::|||||
Db    760  GTTGGCTATCACACCCGCTGGATAGAA---CATGTTCATGTGATTCAGCCA-----  807

Qy    669  ProProAspSerGlyProLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAla---  687
                  |:::||:|||
Db    808  ------------CGGAGCAGAGCTGCCATTGAGTGCCATCTCTG  840

Qy    688  SerAspThrAsp  691
                  |||||||
Db    841  GAAGTGCTCTCCGACCAGGAGAGAGGAGACAGCAATGTGGTGTTAAAAATGATGAAAGT  900

Qy    692  GlyLeuAspSerValGluAlaAlaAlaAlaProProIleLeuSerSerVal---Glu  710
                  ||:|:
Db    901  AGCAGCTCATCATCCATTATCTTTGCTGAGCCCACCCCAGAAAAGAAAAAACGCTTTGGAGAA  960

Qy    711  TrpSerThrSerGlyLeuArgSerAlaSerAlaArgPheProAla------ThrGlyPro  728
                  :|:|||:
Db    961  TCTGACACTGAAAATCAGAATAACAAGTCGGTGAAGTACACCACCAATTTAGTCATAAGA 1020

Qy    729  GlySerSerAspSerAspSerAspSerGluAspAspAspGluHisGlyGlyValPheSerGlnSer  748
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Db   1021  GAATCTGGTGACTTGAGTCGAGCTCCAGGAAAATGCTTGGCTGGTTTGTCT 1080

Qy    749  PheLeuProAlaSerSerGluSerAspIleIlePheAspAsnGluAspAsnGlnGluAsnSer  768
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Db   1081  ------GCCAGTTCAATGTGGAACAGCAGTCGCCACTCAGGCGTAATCCCACCTAGAG 1134

Qy    769  LysSerGlnAsnGlnAspCysAsnGluGluValGlyCysHisGluSerGluPro  788
                  ::|:|:|||:|||||:
Db   1135  GAGAGTTTCACATCCACGGAAGAAATTCCGAAGAAAATGTCAACTTTTGGGTCAG-- 1191

Qy.   789  SerValThrGlnAlaValHisTyr------LeuTyrIleGlnMetGluTyrCysGlu  806
                  :::|:|::
Db   1192  ---ACAGAGGCACAGTACCACCCTGATGTGCACATCCAGATCCAGCTGTGTGAG 1242

Qy    807  LysSerThrLeu------ArgAspThrIleAspGln  816
                  :::||:
Db   1243  CTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAGCCGGGGCCGGAGTATGTGACGAG 1302

Qy    817  GlyLeu------TyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAsp  834
                  :::::||:|||||||:|:::::::||
Db   1303  TCTGCCTGTCCTTATGTTATGGCCAATGTTGCAACAAAAAATTTTCAAGAATTGGTAGAA 1362

Qy    835  GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle  854
                  ||:||:|:|||||||:
Db   1363  GGTGTGTTTTACATACATAACATGGGAATTGTGCACCGAGATCTGAAGCCAAGAAATATT 1422

Qy    855  PheLeuAspSer--AspAspHisValLysIleGlyAspPheGlyLeuAla--ThrAsp  872
                  ||||||      ||||||
Db   1423  TTTCTTCATGGCCCTGATCAGCAAGTAAAAATAGGAGACTTTGGTCTGGCCTGCCACGAC 1482
```

```
Y     873  HisLeuAlaPheSerAlaAspAspGlnThrGlyAspLeuIleLeuLysSer  892
           |||                        |||||||||||||||||||||||
b    1483  ATCCTA-------------------CAGAAGAACACAGACTGGACAACAGAAACGGGAAGAGA  1527

Y     893  AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu---  911
           ||||||:::                |||                 |||||
b    1528  ACACCAACA---CAT--ACGTCCAGAGTGGGTACTTGTCTGTACGCTTCACCCGAACAG  1581

Y     912  ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle  931
           :::::::                   |||
b    1582  TTGGAAGGA-------------TCTGAGTATGATGCCAAGTACAGATATGTACAGCTTGGGTGTG  1632

Y     932  IlePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu  951
           ::::|||                   :::||||||
b    1633  GTCTGCTAGAGCTC---TTTCAGCCGTTTGAACAGAAAATGGCCGGAGCAGAAGTTCTA  1689

Y     952  AsnGlnLeuArgAspProThrSerProLysPheAspPheAspAspGlyGluHis  971
           |||||                     :::   |||
b    1690  ACAGGTTAAGA-------ACTGGTCAGTTGCCGGAATCCCTCCGTAAA---AGGTGT  1737

Y     972  AlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThr  991
           |||                       :::   :::::|||:::|||
b    1738  CCAGTGCCAAGCCAAGTATATCCAGCACTTAACGAAGGAACTCATCCGCAGAGACCCATCT  1797

Y     992  AlaThrGluLeuLeuLysSerGluLeu 1000
           |||           :::
b    1798  GCCATTCAGCTGCTGCAGAGTGAACTT  1824
```

RESULT 7
US-09-016-434-785
Sequence 785, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
  APPLICANT: Janice Au-Young
  APPLICANT: Jeffrey J. Seilhamer
  TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
  TITLE OF INVENTION: PATHWAY GENE EXPRSSION
  NUMBER OF SEQUENCES: 1490
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
    STREET: 3174 PORTER DRIVE
    CITY: PALO ALTO
    STATE: CALIFORNIA
    COUNTRY: USA
    ZIP: 94304
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/016,434
    FILING DATE: HEREWITH
    CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:
    FILING DATE:
    CLASSIFICATION:
  ATTORNEY/AGENT INFORMATION:
    NAME: Zeller, Karen J.
    REGISTRATION NUMBER: 37,071
    REFERENCE/DOCKET NUMBER: PA-0002 US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (650) 855-0555
    TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 785:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 244 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  IMMEDIATE SOURCE:
    LIBRARY: HNT2AGT01

;   CLONE: 488190
US-09-016-434-785

Alignment Scores:
Pred. No.:   1.14e-36   Length: 244
Score: 443.00   Matches: 81
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 5.18%   Indels: 0
DB: 4   Gaps: 0

US-09-515-806A-2 (1-1649) x US-09-016-434-785 (1-244)

```
Qy    771  GlnAsnGlnAspGluAspCysAsnGlyLysAsnGlyCysHisGluSerGluProSerVal  790
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  CAGAATCAGGATGAAGATTGCAATGAAAGAAGAAATGGCTGCCATGAGAAAGTGAGCCATCAGTG  60

Qy    791  ThrThrGluAlaValHisTyrIleLeuTyrIleGlnMetGluTyrCysGluLysSerThrLeu  810
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ACGACTGAGGCTGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTTA  120

Qy    811  ArgAspThrIleAspGlnGlyLeuTyrArgAspThrValArgLeuTrpValArgLeuPheArg  830
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  CGAGACACCATTGACCAGGGACTGTATCGAGACACCGTGAGACTCTGGGAGGCTTTTCGA  180

Qy    831  GlyIleLeuAspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLys  850
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GAGATTCTGGATGGATTAGCTTATATCCATGAGAAAGGAATGATTCACCCGGATTGAAG  240

Qy    851  Pro 851
Db    241  CCT 243
```

RESULT 8
US-08-143-219-1
; Sequence 1, Application US/08143219
; Patent No. 5670330
; GENERAL INFORMATION:
;   APPLICANT: Sonenberg, Nahum
;   APPLICANT: Katze, Michael G.
;   APPLICANT: Roy, Sophie
;   APPLICANT: Koromilas, Antonis E.
;   APPLICANT: Barber, Glen N.
;   TITLE OF INVENTION: TUMOR-CELL ASSAY METHOD AND KIT
;   NUMBER OF SEQUENCES: 27
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Lyon & Lyon
;   STREET: 611 West Sixth Street
;   CITY: Los Angeles
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 90017
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;   COMPUTER: IBM compatible
;   OPERATING SYSTEM: PC-DOS (Version 5.0)
;   SOFTWARE: WordPerfect (Version 5.1)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/143,219
;   FILING DATE: October 25, 1993
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA: including application
;   PRIOR APPLICATION DATA: described below:
;   APPLICATION NUMBER: 08/141,244
;   FILING DATE: October 22, 1993
;   APPLICATION NUMBER: 07/953,681
;   FILING DATE: September 29, 1992
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Douglas E. Olson
;   REGISTRATION NUMBER: 22,798
;   REFERENCE/DOCKET NUMBER: 204/139
;   TELECOMMUNICATION INFORMATION:

two

```
TELEPHONE:  (213) 489-1600
TELEFAX:    (213) 955-0440
TELEX:      67-3510
INFORMATION FOR SEQ ID NO:  1:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 2628 base pairs
   TYPE: nucleic acid
   STRANDEDNESS: double
   TOPOLOGY: linear
   MOLECULE TYPE: DNA (genomic)
   HYPOTHETICAL: NO
   ORIGINAL SOURCE:
   INDIVIDUAL ISOLATE: HUMAN PKR GENE, FIGURE 5
   FEATURE:
      NAME/KEY: CDS
      LOCATION: 187..1836
IS-08-143-219-1
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Alignment Scores:
Pred. No.:               2628
Score:           5.55e-32       Matches:           416.00
Percent Similarity:  37.10%     Conservative:      179
Best Local Similarity: 24.97%   Mismatches:         87
Query Match:          4.87%     Indels:            197
DB:                      1      Gaps:              255
                               Gaps:               31
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IS-09-515-806A-2 (1-1649) x US-08-143-219-1 (1-2628)

Qy    329  GlyLysGluLysIleAspLysCysLysGlyGlnIleGlyGlnThrGluPheAsn  348
           ||||||||:||:::||::::|:||:|||::||||
Db    344  CAGAAGGTGAAGGTAGATCAAAGAAGAAGCAA----------------------  376

Qy    349  SerLeuValLysLeuSerHisProAsn---ValValArgTyrLeuAlaMetAsnLeuLys  367
           |||||::|||||   ::|||:|||||||||||
Db    377  -------AAAATGCCGCAGCCAAATTAGCTGTTGAGATACTTAATAAGGAAAAGAAGG  427

Qy    368  GluGlnAspAspSerIleValValAspIleLeuValGluHisIleSer------GlyVal  385
           :::|                          |||||||||
Db    428  CAG-------------TTAGTCCTTTA-TTATTGACAACAACGAATTCTTCAGAAGGATTA  474

Qy    386  SerLeuAlaAlaHisLeuSerHisSerGlyProIleProValHisGlnLeuArgArgTyr  405
           ||:::::::|                        ::|||
Db    475  TCCATGGGAATTACATAGGCCTTATCAATAGAATTGCC------CAGAAGAAAAGACTA  528

Qy    406  ThrAla--------GlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValVal  422
           |||||          ||||||
Db    529  ACTGTAAATAATGAACAGTGTGCATCGGGG---GTGCATGGGCCCAGAAGGATTT  579

Qy    423  His-----------------------------  423
           |||
Db    580  CATTATAAATGCAAAATGGGACAGAAAGAATTAGTATTGGTACAGGTTCTACTAAACAG  639

Qy    424  -------LysValLeuSerAlaSerAsnVal------------LeuValAspAlaGlyLeuThr  438
                  |::|||                             ::|||
Db    640  GAAGCAAAACAATTGGCCGCTTAAACTTGCATATCTTCAGATATTATCAGAAGAAACCTCA  699

Qy    439  ValLysIleThrAspTyrSerIleSerArgLeuAlaAspIleAlaCysGluLysAspVal  458
           |:::|||        :|||||
Db    700  GTGAAA------TCTGACTACCTGTCCTCTCGGTTCTTTGCCTACACGTGTGAGTCC----  750

Qy    459  PheGluGlnThrArgValArgPheAspAspAsnArgAlaLeuProTyrLysThrGlyLysLys  478
           :::                            ||||||:::::|||
Db    751  -----------------------CAAAGCAACTCTTTAGTGACCAGCACA----------  777

Qy    479  GlyAspValTrpArgLeuGlyLeuLeuLeuLeuSerGlnGlnGluCysGly  498
           ::|                           |||||:::|
Db    778  -----------CTCGCTTCGAATCATCATCTGAAGGT-----------  804

Qy    499  GluTyrProValThrIleProSerAspLeuProGlnAlaAspPheGlnAspPheLeuLysLys  518
           :|:::|||||                          ||| ::: ||
Db    805  --------GACTTCTCAGCAGATACAATCATCAGAGATAATCTAC---  837

Qy    519  CysValCysLeuAspLysLysGluArgTrpSerProGlnAsnLeuLeuLysLeuHisSerPhe  538
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```
Db    838  ----------------AGTGACAGTTAAACAGTTCTTCGTTGCTTATGAATGGTCTC  879
                                 ::: |||||
Qy    539  IleAsnProGlnProLysMetProLeuValGluGlnSerProGlySerGlyGlyGln  558
           |||  |||  |||
Db    880  AGAAATAATCAAAGGAAGGCAAA-----------------------------  903

Qy    559  AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAlaPhePheSerGlu  578
           ::::::||
Db    904  -------AGATCTTTGGCACCCAGATTTGACCTTCCTGAC---------ATGAAAGAA  945

Qy    579  ThrGlnArgGlnPheSerArgTyrPhe---IleGluPheGluGlnLeuGlnLeuGluGly  597
           ||||:::       :::   :::|||||||:::||
Db    946  ACAAAGTATACTGTGGACAAGAGGTTTGGCATGGATTTTAAAGAAATAGAATTAATTGGC  1005

Qy    598  LysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysCysTyrAla  617
           |||||||||
Db    1006 TCAGGTGGATTTGGCCCAAGTTTCAAAGCAAAACAGAATTGACGAAAGACTTACGTT  1065

Qy    618  ValLysArgIleProIleAsnProAlaSerArgGlnPheArgArgIleLeuGlyGluVal  637
           ::|||||||::|        :::   |||   |||
Db    1066 ATTAAACGTGTTAAATATAATAAC-----------GAGAAGGCCGAGCCGTGAAGTA  1110

Qy    638  ThrLeuLeuSerArgLeuHisHisGluAsnIleValArgTyrTyrAsnAlaTrpIleGlu  657
           |||||| :::||::||||     |||||
Db    1111 AAAGCATTGGCAAAACTTGATCATGTAAAATATTGTTCACTACAATGGCTGTTGG----  1164

Qy    658  ArgHisGluValArgProAlaGlyTyrProGlyProProProAspSerGlyProLeuAlaLys  677
           |||
Db    1164 -----------------------------------------------------  1164

Qy       AspAspArgAlaAlaArgGlyValGlnProAlaSerAspThrAspGlyLeuAspSerValGlu  697
Db    678 ----------------------------------------GATGGATTGAT----  697

Qy       AlaAlaAlaAlaProProProIleLeuSerSerSerValGluTrpSerGlyGluArg  717
Db    1165 ----------------------------------------CTTGAGCAGT--  1176

Qy    698  SerAlaSerAlaArgPheProAlaThrGlyProGlySerAspAspAspGluAspAspAsp  718
           :::|                              :::|
Db    1176 -----------------TATGATCCTGAGACCAGTGATGATCT------------  1203

Qy    718  GluAspGluHisGlyGlyValPheSerGlnSerPheLeuProAlaSerAspSerGluSer  738
Db    1177 ------------------------------GATGGATTGAT----------  1203

Qy    738  AspIleIlePheAspAsnGluAspGlyLnAsnSerLysSerGlnAsnAsnAspGluAspCys  758
           |||
Db    1204 ------------------------------CTTGAGCAGT----  1215

Qy    758  AsnGluLysAsnGlyCysHisGluSerGluProSerValThrThrGluAlaValHisTyr  778
Db    1216 ------------GATTATGATCCTGAGACACAGCAAAAATAGTTCAAGG----  1251

Qy    778  LeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIleAsp--  798
Db    1252 ---TCAAAGACTAAGTGC----------------------------------  1266

Qy    798  GlnGlyLeuTyrArgAspThrValArgLeuTrpArgLeuGluIleLeuAspGly  816
           |||||                      ||||||
Db    1267 CTTTTCATCCAAATTGGAATTCTGTGATAAAGGACCTTGGAACAATGATTGAAAAAGGA  1326

Qy    816  LeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIlePhe  836
           |||      ||||||        ||||||
Db    1327 AGAGGCGAGAAACTAGACAAAGTTTGGCTTTGAACTCTTTGAACAAATAACAAAAGGG  1386

Qy    836  AsnGluLysAsnGlyCysHisGluSerGluProSerValThrThrGluAlaValHisTyr  855
Db    1387 GTGGATTATATACATTCAAAAAATTAATTCATAGAGATCTTAAGCCAAGTATATATTC  1446

Qy    856  LeuAspSerAspHisValLysIleGlyAspPheGlnLeuValLeuAlaThrAspHisLeuAla  875
Db    1447 TTAGTAGATACAAAACAAGTAAAGATTGGAGACTTTGGACTTGTAACATCT-----  1497

Qy    876  PheSerAlaAspSerLysGlnAspThrGlyAspLeuIleLeuSerSerAspProSer  895
           ||||||:::||
Db                 ||||
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Pred. No.:                              Length:          2562
Score:                     9.59e-32     Matches:          179
Percent Similarity:         413.50      Conservative:      87
Best Local Similarity:      37.10%      Mismatches:       198
Query Match:                24.97%      Indels:           254
DB:                          4.84%      Gaps:              31
                                2

US-09-515-806A-2 (1-1649) x US-08-436-771-8 (1-2562)

Qy  329 GluLysGluLysIleAspLysCysLysLysIleGlnIleGlnGlyThrGluThrGluPheAsn 348
            :::|||||||:::|||:|:||:||
Db  344 CAGAAGGTGAAGGTAGATCAAAGAAGGAAGCAA 376

Qy  349 SerLeuValLysLeuSerHisProAsn--ValValArgTyrLeuAlaMetAsnLeuLys 367
           ||:||                     :||||:||||
Db  377 ----AAAATGCCCAGCCAAATTAGCTGTTGAGATACTTAATAAGGAAAAAAGAGG 427

Qy  368 GluGlnAspAspSerIleValValAspIleLeuValGluHisIleSer----GlyVal 385
           ::|||:::                ||||:::||
Db  428 CAG------TTAGTCCTTA-TTAATTGACAACAACGAATTCTTCAGAAGGATTA 474

Qy  386 SerLeuAlaAlaHisIleLeuSerHisSerGlyProIleProValHisGlnLeuArgArgTyr 405
           |||:::                  :::|||
Db  475 TCCATGGGGAATTACATAGGCCTTATCAATAGAATTGCC----CAGAAGAAAAGACTA 528

Qy  406 Thr.Ala--------GlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValVal 422
           |||:::                  :::|||
Db  529 ACTGTAAATTATGAACAGTGTGCATCGGGG----------GTGCATGGGCCAGAAGGATTT 579

Qy  423 His 423
           |||
Db  580 CATTATAAATGCAAAATGGACAGAGAAGAAGAAATATAGTATTGGTACAGTTCTACTAAACAG 639

Qy  424 ----LysValLeuSerAlaSerGluAsnVal------------LeuValAspAlaGluGlyThr 438
           |||                     :::::||
Db  640 GAAGCAAAACAATTGGCCGCTAAACTGCATATCTTCAGATATTATCAGAAGAAACCTCA 699

Qy  439 ValLysIleThrAspTyrSerIleSerGluSerArgLeuAlaAspIleCysLysGluAspVal 458
           ||:::                   :::|||
Db  700 GTGAAA--TCTGACTACCTGCCTCTGGTCTTTGCTACTACGTGTGAGTCC---------- 750

Qy  459 PheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLysLys 478
           |||                     |||:::
Db  751 ----CAAAGCAACTCTTTAGTGACCAGCACA-------------- 777

Qy  479 GlyAspValTrpArgLeuGlnLeuLeuLeuSerLeuSerGlnGlyGlnGluCysGly 498
           |||                     |||
Db  778 ------------CTGCTTCTGAATCATCATCTGAAGGT----------- 804

Qy  499 GluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeuLeuLys 518
           |||:::                  ||||
Db  805 ------------GACTTCTCAGCAGATACATCAGAGATA---------- 831

Qy  519 CysValCysLeuAspLysAspSerGluArgTrpSerProGlnGlnIleLeuLysHisSerPhe 538
           :::                     :::
Db  832 ------AATTCTAACAGTGACAGTTTAAACAGTTCTTCGTTGCTTATGAATGGTCTC 882

Qy  539 IleAsnProGlnProLysMetProLeuValGluGlnSerProGluAspSerGlyGlyGln 558
           |||                     :::
Db  883 AGAAATAAATCAAAGGAAGGCAAAA------------------ 906

Qy  559 AspTyrValGluThrValIleProSerGluAsnArgLeuProSerAlaAlaPhePheSerGlu 578
           |||:::                  :::|||
Db  907 ------AGATCTTTGCACCCAGATTTGACCTTCCTGAC--------ATGAAAGAA 948

Qy  579 ThrGlnArgGlnPheSerArgTyrPhe---IleGluPheGluGlnLeuLeuGlyLeuGln 597
           |||:::                  ||:::
Db  949 ACAAAGTATATCGTGACAAGAGGTTTGGCATGTGGATTTAAAGAAATAGAATTAATTGGC 1008

Qy  598 LysGlyAlaPheGlyAlaValIleLeuValGlnAsnLeuAsnLeuValGlyCysTyrAla 617
           |||                     |||
Db 1009 TCAGGTGGATTTGGCCAAGTTTTCAAAGCAAACACCAGAAATTGACGGAAAGACTTACGTT 1068
```

```
Db 1498 ----------CTGAAAAATGAT------ 1509
Qy  896 GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnGlySer 915
            |||          ||:::|||||
Db 1510 GGAAAGCGAACAAGGAGTAAGGAACTTTGCGATACATGAGCCCAGAACAGATTCTTCG 1569
Qy  916 ThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIleIlePhePheGlu 935
            :::::
Db 1570 ------CAAGACTATGGAAAGGAAGTGGACCTCTACGCTTTGGGGCTAATTCTTGCTGAA 1623
Qy  936 MetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeuArg 955
            :::          |||
Db 1624 CTT---CTTCATGTGATGTGACACTGCTTTGAAACATCAAAGTTTTCACAGACCTACGG 1680
Qy  956 AspProThrSerProLysPheAspPheAspLysGlyHisGluHisAlaLysAlaLysGlnLys 975
            |||          :::
Db 1681 GATGGCATC----------ATCTCAGATATATTTGAT------------------AAAAAAGAAAAA 1719
Qy  976 SerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu 995
            :::::::
Db 1720 ACTCTTCTACAGAAATTACTCTCAAAGAAACCTGAGGATGGACCTAACACATCTGAAATA 1779
Qy  996 LeuLysSerGluLeuLeuProProProGlnMetGluGluSerGluLeuHis 1012
            |||:::          :::::::
Db 1780 CTAAGGACCCTTGACTGTGTGGAAGAAAAGCCCAGAGAAAAATGAACGACAC 1830
```

```
Qy   618  ValLysArgIleProIleAsnProAlaSerArgGlnPheArgArgIleLysGlyGluVal 637
          :::|||||||::                 :::        :||||||
Db  1069  ATTAAACCGTGTAAATAATAAATAAC-------GAGAAGGCGGAGCGTGAAGTA 1113

Qy   638  ThrLeuLeuSerArgLeuHisHisGluAsnIleValArgTyrTyrAsnAlaTrpIleGlu 657
          ||||:::::|||  ||| |||||           |||
Db  1114  AAAGCATTGGCAAAACTTGATCATGTAAATATGTTCACTACAAATGGCTGTTGG----- 1167

Qy   658  ArgHisGluArgProAlaGlyProGlyThrProProAspSerGlyProLeuAlaLys 677
Db  1167  ------ 1167

Qy   678  AspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyGlySerValGlu 697
                                                      ||||| |||
Db  1168  ------GATGGATTGAT----- 1179

Qy   698  AlaAlaAlaProProIleLeuSerSerSerValGluTrpSerThrSerGlyGlyArg 717
Db  1179  ------ 1179

Qy   718  SerAlaSerAlaArgPheProAlaThrGlyTyrGlySerSerAspAspGluAspAspAsp 737
          |||||||                ||||||||||||
Db  1180  ------TATGATCCTGAGACCAGTGATGATTCT---- 1206

Qy   738  GluAspGluHisGlyGlyValPheSerGlnSerPheLeuProAlaSerAspSerGluSer 757
                                                      ||| :::|||
Db  1207  CTTGAGGCAGT----- 1218

Qy   758  AspIleIlePheAspAsnAsnSerLysSerGlnAsnGlnAsnAspGluAspCys 777
                 :::                |||||||||
Db  1219  ------GATTATGATCCTGAGAACAGCAAAATAGTTCAAGG----- 1254

Qy   778  AsnGluLysAsnGlyCysHisGlySerGluProSerValThrThrGluAlaValHisTyr 797
          |||||                                  |||
Db  1255  ---TCAAAGACTAAGTGC--- 1269

Qy   798  LeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIleAsp----- 815
          |||:::|||||||                          ||||::||
Db  1270  CTTTTTCATCCAAATGGAATTCTGTGATAAAGGACCTTGAACAATGGATTGAAAAAAAGA 1329

Qy   816  GlnGlyLeuTyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAspGly 835
          ||||                   :::|                 ||||||||||:::|||
Db  1330  AGAGGCGAGAAACTAGACAAAGTTTGGCTTTGAACAAATAACAAAAGGG 1389

Qy   836  LeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIlePhe 855
          :::                    ::|||||               ||||||||
Db  1390  GTGGATTATATACATTCAAAAAAATTAATTCATAGAGATCTTAAGCCAAGTATATATTC 1449

Qy   856  LeuAspSerAspHisValLysIleGlyAspPhePheLeuAlaThrAspHisLeuAla 875
          |||                    ||||||||||||
Db  1450  TTAGTAGATACAAAACAAGTAAAGATTGGAGACTTTGGACTTGTAACATCT------- 1500

Qy   876  PheSerAlaAspSerLysSerGlnAspAspGlnThrGlyAspLeuLeuIleLysSerAspProSer 895
          :::|||||||:::|||
Db  1501  ------CTGAAAAATGAT----- 1512

Qy   896  GlyHisGlyLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnGlySer 915
          ::| |||                    :||||||
Db  1513  GGAAAGGCGGACAAGGAGTAGGGGAACTTTCGCGATACATGAGCCCCAGAACAGATTTCTTCG 1572

Qy   916  ThrLysSerAlaTyrAsnGlnLysValAspSerLeuPheSerLeuGlyIleIlePhePheGlu 935
          |||                    ::||||||||||||
Db  1573  ------CAAGACTATGGAAAGGAAGTGGACCTCTACGCTTTGGGGCTAATTCTTGCTGAA 1626

Qy   936  MetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeuArg 955
          :::                    |||||||||||||
Db  1627  CTT---CTTCATGTATGTGACACTGCTTTTGAAACATCAAAGTTTTCACAGACCTACGG 1683

Qy   956  AspProThrSerProLysProPheProGluAspProAspAspGlyHisAlaLysGlnLys 975
          |||                    |||||||||||||
Db  1684  GATGGCATC--------ATCTCAGATATATTTGAT---------AAAAAGAAAAA 1722

Qy   976  SerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThrLeuThrGluLeu 995
          :::                    |||
```

```
Db  1723  ACTCTTCTACAGAAAATTACTCTCAAAGAAACCTGAGGATCGACCTAACCATCTGAAATA 1782
          ::::|||::|                        :::||||||
Qy   996  LeuLysSerGluLeuLeuProProProGlnMetGluGluSerGluLeuHis 1012
          |||::::|||                        |||::::|||
Db  1783  CTAAGGACCTTGACTGTGTGGAAGAAAAGCCCAGAGAAAATGACGACAC 1833
```

RESULT 10
US-08-434-998-8

; Sequence 8, Application US/0434998
; Patent No. 5866781
GENERAL INFORMATION:
;   APPLICANT: Silverman, Robert H.
;   APPLICANT: SenGupta, Dibyendu N.
;   TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
;   TITLE OF INVENTION: Cells and Methods
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;   ADDRESSEE: Russell
;   STREET: 200 E. Broward Boulevard
;   CITY: Fort Lauderdale
;   STATE: Florida
;   COUNTRY: USA
;   ZIP: 33301
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/434,998
;   FILING DATE:
;   CLASSIFICATION: 800
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/198,973
;   FILING DATE: 18-FEB-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Manso, Peter J.
;   REGISTRATION NUMBER: 32,264
;   REFERENCE/DOCKET NUMBER: CL11363-16
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 305/527/2498
;   TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2562 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-08-434-998-8

```
Alignment Scores:
Pred. No.:                                    Length:              2562
Score:              9.59e-32                  Matches:              179
Percent Similarity: 413.50                    Conservative:          87
Best Local Similarity: 37.10%                 Mismatches:           198
Query Match:        24.97%                     Indels:               254
DB:                 4.84%                      Gaps:                  31
                    2
US-09-515-806A-2 (1-1649) x US-08-434-998-8 (1-2562)
```

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Qy   329  GluLysGluLysIleAspLysCysLysLysGlnIleGlnGlyThrGluThrGluPheAsn 348
          :::|||||||||                ::|||||
Db   344  CAGAAGGTGAAGGTAGATCAAAGAAGGAAGCAA------------------------ 376

Qy   349  SerLeuValLysLeuSerHisProAsn---ValValArgTyrLeuAlaMetAsnLeuLys 367
          :::                    ::||||||
Db   377  --------AAAATGCCGCAGCCAAATTAGCTGTTGAGATACTTAATAAGGAAAAGAGG 427

Qy   368  GluGlnAspAspSerIleValValAspIleLeuValGluHisHisIleSer------GlyVal 385
          :::                    |||                     |||
```

RESULT 11
US-08-487-797-8
Sequence 8, Application US/08487797
Patent No. 5866787
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: SenGupta, Dibyendu N.
TITLE OF INVENTION: Transgenic Plants Co-Expressing A
TITLE OF INVENTION: Functional Human 2-5A System
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Holland & Knight

```
STREET:  One E. Broward Boulevard, #1100
CITY:  Fort Lauderdale
STATE:  Florida
COUNTRY:  USA
ZIP:  33301
COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/487,797
    FILING DATE:  07-JUNE-1995
    CLASSIFICATION:  800
ATTORNEY/AGENT INFORMATION:
    NAME:  Manso, Peter J.
    REGISTRATION NUMBER:  32,264
    REFERENCE/DOCKET NUMBER:  CL11363-16(C)
TELECOMMUNICATION INFORMATION:
    TELEPHONE:  305/468-7811
    TELEFAX:  305/463-2030
INFORMATION FOR SEQ ID NO:  8:
SEQUENCE CHARACTERISTICS:
    LENGTH:  2562 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
MOLECULE TYPE:  cDNA

US-08-487-797-8

Alignment Scores:
Pred. No.:                        9.59e-32          Length:          2562
Score:                            413.50            Matches:         179
Percent Similarity:               37.10%            Conservative:    87
Best Local Similarity:            24.97%            Mismatches:      198
Query Match:                      4.84%             Indels:          254
DB:                               2                 Gaps:            31

US-09-515-806A-2 (1-1649)  x  US-08-487-797-8 (1-2562)

Qy      329  GluLysGluIleAspLysLysCysLysLysGlnIleGlnGlyThrGluPheAsn  348
                         |||| |||||
Db      344  CAGAGGGTGGAAGGTAGATCAAAGAAGGAAGCAA------------------------  376

Qy      349  SerLeuValLysLeuSerHisProAsn--ValValArgTyrLeuValMetAsnLeuLys  367
                    :|:|:|    |||||||  ::::||||  :|:|||| ||:|
Db      377  --------AAAATGCCGCAGCCAAATTAGCTGTGTGAGATACTTAATAAGGAAAAGAAGG  427

Qy      368  GluGlnAspAspSerIleValAlaAspIleLeuValGluHisIleSer------GlyVal  385
                    ::::|:|    :::||     :::|:|
Db      428  CAG--------------TTAGTCCTTTA-TTATTGACAACAACGAATTCTTCAGAAGGATTA  474

Qy      386  SerLeuAlaAlaHisLeuSerHisGlyProIleProValHisGlnLeuArgArgTyr  405
                    ||:|:|||||| |||||||| :::||
Db      475  TCCATGGGGAATTACATAGGCCTTATCAATAGAATTGCC-------CAGAGAAAAGACTA  528

Qy      406  ThrAla-------GlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValVal  422
                 |||                   ||||||   ::::|||
Db      529  ACTGTAAATTATGAACAGTGTGCATCGGG-------GTGCATGGGGCCAGAAGGATTT  579

Qy      423  His                                                       423
                 ||||
Db      580  CATTATAAATGCAAAATGGGACCAGAAGAATATAGTATTGGTACAGGTTCTACTAAACAG  639

Qy      424  ------LysValLeuSerAlaSerAsnVal-------LeuValAspAlaGluGlyThr  438
                       ||||||||      :::|||       :::::||
Db      640  GAAGCAAAACAAACAATTGGGCCGCTAAACTTCATCTTCAGATATTATCAGAAGAAACCTCA  699

Qy      439  ValLysIleThrAspThrTyrSerIleSerArgLeuAlaAspIleCysLysGluAspVal  458
                 ||| ||||||||||||||||||  ||||||||||
Db      700  GTGAAA---TCTGACTACCTGTCCTCTGGTTCTTTTGCTACTACCGTGTGAGTCC------  750

Qy      459  PheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLysLys  478
                 |||
```

```
Db      751  ---------------------------------------CAAAGCAACTCTTTAGTGACCAGCACA-------  777
                                                      |||:::|||
Qy      479  GlyAspValTrpArgLeuGlyLeuLeuLeuSerLeuSerGlnGlyGlnGluCysCysGly  498
                    |||||
Db      778  CTCGCTTCTGAATCATCATCTGAAGGT--------------------------  804

Qy      499  GluTyrProValThrIleProSerArgAspPheGlnAsnPheLeuAsnLeuLys  518
                    ||||||
Db      805  GACTTCTCAGCAGATACATCAGAGATA--------------------  831

Qy      519  CysValCysLeuAspAspLysGluArgTrpSerProGlnGlnLeuLeuLysHisSerPhe  538
                 :::    :|::|||||
Db      832  ---AATTCTAACAGTGACAGTTAAACAGTTCTTCGTTGCTTATGAATGGTCTC  882

Qy      539  IleAsnProGlnProLysMetProLeuValGluValGlnLeuSerProGluAspSerGlyGlyGln  558
                 |||||||
Db      883  AGAAATAATCAAAGGAAGGCAAAA------------------------  906

Qy      559  AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAlaPheSerGlu  578
                 ||||||
Db      907  ----------AGATCTTTGGCACCCAGATTTGACCTTCCTGAC----ATGAAAGAA  948

Qy      579  ThrGlnArgGlnPheSerArgTyrPhe--IleGluPheGluLeuGlnLeuLeuGly  597
                 |||:::    :|:|:||::||||||||::|:|
Db      949  ACAAAGTATACTGTGGACAGGAGTTTGGCATGAGTTTAAAGAAATAGAATTAATTGGC  1008

Qy      598  LysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysCysTyrAla  617
                 |||
Db      1009 TCAGGTGGATTGGCCAAGTTTCAAAGCAAAACACAGAATTGACGGAAAGACTTACGTT-----  1068

Qy      618  ValLysArgIleProIleAsnProAlaSerArgGlnPheArgIleLysGlyGluVal  637
                 :::|||||||:::    :::  ||||
Db      1069 ATTAAACGTGTTAAATAATAAC---------GAGAAGGCGGAGCGTGAAGTA  1113

Qy      638  ThrLeuLeuSerArgLeuHisHisGluAsnIleValArgTyrTyrAsnAlaTrpIleGlu  657
                 |||    |:::|||||||||| ||||||||||||||::::|||
Db      1114 AAAGCATTGGCAAAACTTGATCATGTAAATATTGTTCACTACAATGGCTGTTGG------  1167

Qy      658  ArgHisGluArgProAlaGlyProGlyThrProProAspSerGlyProLeuAlaLys  677
                 |||
Db      1167 -------------------------------------------------------------  1167

Qy      678  AspAspArgAlaAlaArgGlyGlnProAlaSerArgAspThrAspGlyLeuAspSerValGluGlu  697
                 |||
Db      1168 ---------------------------------------------GATGGATTGAT  1179

Qy      698  AlaAlaAlaProProIleLeuSerSerSerValGluTrpSerThrSerGlyGluArg  717
                 |||
Db      1179 -------------------------------------------------------------  1179

Qy      718  SerAlaSerAlaArgPheProAlaThrGlyProGlySerSerAspAspGluAspAspAsp  737
                 |||
Db      1180 -----------------------TATGATCCTGACACCAGTGATGATTCT---------  1206

Qy      738  GluAspGlyHisGlyGlyValPheSerGlnSerPheLeuProAlaSerAspSerGluSer  757
                 |||              :::|||||
Db      1207 -----------------------------------CTTGAGAGCAGT-------------  1218

Qy      758  AspIleIlePheAspAsnGluAspAsnSerLysSerGlnAsnGlnAspGluAspCys  777
                 |||
Db      1219 -----------GATTATGATCCTGAGAACAGCAAAAATAGTTCAAGG  1254

Qy      778  AsnGluLysAsnGlyCysHisGlySerGluSerGluProSerValThrGluAlaValHisTyr  797
                 |||                  :::::||||
Db      1255 ---TCAAAGACTAAGTGC--------------------------------  1269

Qy      798  LeuTyrArgIleGlnMetGluTyrCysGluLysSerThrLeuArgAspIleAsp-------  815
                 ||||||||||||||||||::::||||||||||||||||||||||
Db      1270 CTTTTCATCCAAATGGAATTCTGTGACAACAATGGATTGGAACATGGATTTGAAAAAAGA  1329

Qy      816  GlnIleLeuTyrArgAspThrValArgLeuPheArgLeuTrpArgLeuPheArgGlyLeuLeuAspGlyVal  835
                 :::|||
```

```
;           TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO:  8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  2562 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
PCT-US95-02058-8

Alignment Scores:
Pred. No.:                9.59e-32        Length:        2562
Score:                    413.50          Matches:       179
Percent Similarity:       37.10%          Conservative:  87
Best Local Similarity:    24.97%          Mismatches:    198
Query Match:              4.84%           Indels:        254
DB:                       5               Gaps:          31

US-09-515-806A-2 (1-1649) x PCT-US95-02058-8 (1-2562)
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```
Qy    329  GluLysGluIleAspLysCysLysLysGlnIleGlnGlyThrGluThrGluPheAsn  348
               ::|||||        |||:|||      :::|||||
Db    344  CAGAAGGTGAAGTAGATCAAAGAAGGAAGCAA                              376

Qy    349  SerLeuValLysLeuSerHisProAsn---ValValArgTyrLeuValAlaMetAsnLeuLys  367
               |||::    :::|||                  :||||
Db    377  ---AAAATGCCCAGCCAAATTAGCTGTTGAGATATTAATAAGGAAAAGAAGG          427

Qy    368  GluGlnAspAspSerIleValAspIleLeuValGluHisIleSer------GlyVal  385
               :::                        ||||
Db    428  CAG-----TTAGTCCTTA-TTATTGACAACAACGAATTCTTCAGAAGGATTA          474

Qy    386  SerLeuAlaAlaHisLeuSerHisSerGlyProIleProValHisGlnLeuArgArgTyr  405
               ||||       :::|||                    CAGAAGAAAGACTA        528
Db    475  TCCATGGGGAATTACATAGGCCTTATCAATAGAATTGCC----

Qy    406  ThrAla---------GlnLeuLeuSerGlyLeuHisSerAsnSerValVal  422
               ||||||
Db    529  ACTGTAAATTATGAACAGTGTGCATCGGGG---------------GTGCATGGGCCGCGAAGAGGATTT  579

Qy    423  His
               |||
Db    580  CATTATAAATGCAAAATGGGACAAAGAAGAAGAATATTAGTATTGGTACAGGTTCTACTAAACAG  639

Qy    424  ------LysValLeuSerAlaSerAsnVal------LeuValAspAlaGluGlyThr  438
               ||||||:||:|            :::::::
Db    640  GAAGCAAAACAAATTGCCCGTAAACTTGCATATCTTCAGATATTATCAGATAATTATCAGAAGAAACCTCA  699

Qy    439  ValLysIleThrAspTyrSerIleSerLysSerArgLeuAlaAspIleCysLysGluAspVal  458
               ||||||                         |||
Db    700  GTGAAA---TCTGACTACCTGCCTCCTCTGGTTCTTTGCTACTACGTGTGAGTCC---  750

Qy    459  PheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLysLys  478
               ||||||                                  |||:|||
Db    751  ----------------CAAAGCAACTCTTTTAGTAGCCAGCCAGCACA---  777

Qy    479  GlyAspValTrpArgLeuGlyLeuLeuLeuLeuSerLeuSerGlnGlnIleGlnGluCysGlyGly  498
               :::||:|||
Db    778  ----------------CTCCCTTCTGAATCATCTGAAGGT-----------  804

Qy    499  GluTyrProValThrIleProSerLeuProAlaAspPheGlnAspPheLeuLysLys  518
               ||||||:::
Db    805  GACTTCTCAGCAGATACATCAGAGATA---  831

Qy    519  CysValCysLeuAspAspLysGluArgTrpSerProGlnGlnLeuLysHisSerPhe  538
               :::    :::                  :::|||
Db    832  ------AATTCTAACAGTGACAGTTTAAACAGTTCTTCGTTGCTTATGAATGGTCTC  882

Qy    539  IleAsnProGlnProLysMetProLeuValGluGlnSerProGluValAspSerGlyGlyGln  558
               |||
Db    883  AGAAATAATCAAAGGAAGGCAAAA---  906

Qy    559  AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAlaPhePheSerGlu  578
```

```
b     1330  AGAGGCCGAGAAACTAGACAAAGTTTGGCTTTGGAACTCTTTGAACAAATAACAAAAGG  1389
y      836  LeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysAspLeuValAsnIlePhe  855
               :::    ||||||||  |||       :::|||
b     1390  GTGGATTATATACTCAAAAAAATTAATTCATAGAGATCTTAAGCCAAGTAATATATATTC  1449
y      856  LeuAspSerAspAspHisValLysIleGlyLysGlyValAlaThrAspPheHisLeuAla  875
               ||||||          ||||||||||
b     1450  TTAGTAGATACAAAACAAGTAAAGATTGGACTTTGGACTTGTAACATCT----------  1500
y      876  PheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSerAspProSer  895
               :::||||:::::||
b     1501  ----------------------CTGAAAATGAT------  1512
y      896  GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnGlyGlySer  915
               |||||||||||||                  |||:||||||
b     1513  GGAAAGGCGAACAAGGAGTAGGGGAACTTTGCCGATACATGAGCCCAGAACAGATTTCTTCG  1572
y      916  ThrLysSerAlaTyrArgAsnGlnLysValAspPheSerLeuGlyIleIleLeuPhePheGlu  935
               :::::::||||||||||:::||||||||
b     1573  ------CAAGACCATGGAAAGGAAGTGGACCCTCCACGCTTTGGGGCTTAATTCTTGCTGAA  1626
y      936  MetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeuArg  955
               :::         |||       |||:::|||
b     1627  CTT---CTTCATGTATGTGACACTGCTTTTGAAACATCAAAGTTTTCACAGACCTACGG  1683
y      956  AspProThrSerProLysProPheProGluAspPheAspAspGlyGluHisAlaLysGlnLys  975
               :::                  :::||||||:::
b     1684  GATGGCATC--------ATCTCAGATATATTTGAT--------AAAAAGAAAAAA  1722
y      976  SerValIleSerTrpLeuLeuAsnHisAspProAlaLysProAlaArgProThrAlaThrGlyLeu  995
               :::::::::::::            ||                      :::|||:::
b     1723  ACTCTTCTACAGAAATTACTCCAAAGAACCTGAGGATCGGACCTAACACATCTGAAATA  1782
y      996  LeuLysSerGluLeuLeuProProProGlnMetGluGlyLeuSerGluGluHis  1012
               ||||||||
b     1783  CTAAGGACCCTTGACTGTGTGGAAGAAAAAGCCCAGAGAAAAATGAACGACAC  1833
```

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RESULT 12
PCT-US95-02058-8
; Sequence 8, Application PC/TUS9502058
; GENERAL INFORMATION:
;   APPLICANT:  Silverman, Robert H.
;   APPLICANT:  SenGupta, Dibyendu N.
;   TITLE OF INVENTION:  Antiviral Transgenic Plants, Vectors,
;   TITLE OF INVENTION:  Cells and Methods
;   NUMBER OF SEQUENCES:  11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Ruden, Barnett, McClosky, Smith, Schuster &
;     ADDRESSEE:  Russell
;     STREET:  200 E. Broward Boulevard
;     CITY:  Fort Lauderdale
;     STATE:  Florida
;     COUNTRY:  USA
;     ZIP:  33301
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US95/02058
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/198,973
;     FILING DATE:  18-FEB-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Manso, Peter J.
;     REGISTRATION NUMBER:  32,264
;   REFERENCE/DOCKET NUMBER:  CL11363-16
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  305/527/2498
```

```
Db   1573  ------CAAGACTATGAAAGGAAGTGGACCTCTACGCTTTGGGGCTAATTCTTGCTGAA 1626
                                                          |||||
Qy    936  MetSerTyrHisProMetValThrLeuSerGluArgIleGluPheValLeuAsnGlnLeuArg 955
             :::                           ::::
Db   1627  CTT---CTTCATGTATGTGACACTGCTTTGAAACATCAAAGTTTTCACAGACCTACGG 1683
             ||||
Qy    956  AspProThrSerProLysPheProLysPheProGluAspPheAspGlyGluHisAlaLysGlnLys 975
                                          :::  ::::        |||||
Db   1684  GATGGCATC------ATCTCAGATATATTTGAT------AAAAAAGAAAAA 1722
             |||
Qy    976  SerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu 995
             :::::::::
Db   1723  ACTCTTCTACAGAAATTACTCTCAAAGAAACCTGAGGATCGACCTAACACATCTGAAATA 1782
             ||||::::
Qy    996  LeuLysSerGluLeuLeuProProGlnMetGluGluSerGluLeuHis 1012
             ||||:::
Db   1783  CTAAGGACCTTGACTGTGTGGAAGAAAAGCCCAGAGAAAATGACGACAC 1833
```

RESULT 13
US-09-554-726A-11
; Sequence 11, Application US/09554726A
; Patent No. 6642369
; GENERAL INFORMATION:
; APPLICANT: HERRMANN, Bernhard
; APPLICANT: KOSCHORZ, Birgit
; APPLICANT: KISPERT, Andreas
; TITLE OF INVENTION: NUCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATION:
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 258.0009 0101
; CURRENT APPLICATION NUMBER: US/09/554,726A
; CURRENT FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: PCT/EP 98/07395
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: EP 98 10 3596.7
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: EP 97 12 0190.0
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 11
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (524)..(1975)
; OTHER INFORMATION:
US-09-554-726A-11

Alignment Scores:
Pred. No.:   Length: 2827
Score: 6.06e-26   Matches: 185
Percent Similarity: 39.90%   Conservative: 123
Best Local Similarity: 23.96%   Mismatches: 254
Query Match: 4.19%   Indels: 212
DB: 4   Gaps: 35

US-09-515-806A-2 (1-1649) x US-09-554-726A-11 (1-2827)

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Qy    345  ThrGluPheAsnSerLeuValLysLeuSerHisProAsnValValArgTyrLeu--Ala 363
             |||::::|:::
Db    674  TCTGAGGCAGAGTTACTGATGATGACCGATCATCCGAATATCATCTCTCCTTCAAGTC 733
Qy    364  MetAsnLeuLysGluGlnAspAspSerIleValAspSerIleLeuValGluHisIleSer 383
             :::                                    ::::|||:::::::::
Db    734  ATTGACACCAAGAAGAAA------GTATACCTCATTATGGAGTTGTGCGAG 778
Qy    384  GlyValSerLeuAlaAlaHisLeuSerHisGlyProValHisGlnLeuArg 403
             ||||:::                              :::
Db    779  GGTAAATCACTTTACCAACACATCCAAAATGCTGGCTACCTGCGAGGACGATGAAGCACGC 838
Qy    404  ArgTyrThrAlaGlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValValHis 423
             ||||   |||         ||||::::
```

```
Db    907  ------AGACTTTGGCACCCAGATTTGACCTTCCTGAC---------ATGAAAGA 948
             ::::::                                       |||
Qy    579  ThrGlnArgGlnPheSerArgTyrPhe---IleGluPheGluGluLeuGlnLeuLeuGly 597
             :::                    :::||||
Db    949  ACAAAGTATACTGTGGACAAGAGGTTTGGCATGCAATGGAATATAGAATTATTGGC 1008
Qy    598  LysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysCysTyrAla 617
             ||||::::
Db   1009  TCAGGTGGATTGGCCAAGTTTCAAGCAAAACACAGAATTGACGAAAGACTTACGTT 1068
Qy    618  ValLysArgIleProIleAsnProAlaSerArgGlnPheArgIlePheLysGlyValVal 637
             ::: ||||:::
Db   1069  ATTAAACGTGTAAAATAATAATAAC------GAGAAGGCGGAGCGGTGAAGTA 1113
Qy    638  ThrLeuLeuSerArgLeuHisHisGluHisIleValArgTyrTyrAsnAlaTrpIleGlu 657
             :::|||||:::
Db   1114  AAAGCATTGGCAAAACTTGATCATGTAAAATATTGTTCACTACAATGGCTGTTGG------ 1167
Qy    658  ArgHisGluArgProAlaGlyProGlyThrProProAspSerGlyProLeuAlaLys 677
Db   1167  ------ 1167
Qy   1167  ------ 1167
Db    678  AspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeuAspSerValGlu 697
             ||||:::
Db   1168  ------GATGGATTTGAT------ 1179
Qy    698  AlaAlaAlaProProIleLeuSerSerValGluTrpSerThrSerGlyGluArg 717
Db   1179  ------ 1179
Qy    718  SerAlaSerAlaArgPheAlaThrGlyProGlySerSerAspAspGluAspAspAspAsp 737
             :::||||:::
Db   1180  ------TATGATCCTGAGACCAGTGATGATCT------ 1206
Qy    738  GluAspGluHisGlyGlyValPheSerGlnSerPheLeuProAlaSerAspSerGluSer 757
             :: :||||
Db   1207  ------CTTGAGCGACAGT------ 1218
Qy    758  AspIleIlePheAspAspGluAspGluAspGlnAsnSerLysSerGlnGlnAsnAspCys 777
             :::||||
Db   1219  ------GATTATGATCCTGAGACAGCAAAAATAGTTCAAGG------ 1254
Qy    778  AsnGluLysAsnGlyCysHisGluSerGluProSerValThrThrGluAlaValHisTyr 797
             :::
Db   1255  ---TCAAAGACTAAGTGC------ 1269
Qy    798  LeuTyrIleGlnMetGluThrTyrCysGluLysSerThrLeuArgAspThrIleAsp---- 815
             ||||::::
Db   1270  CTTTTCATCCAAATGGAATTCTGTGATAAAGGGACCCTTGGAACAATGATTGAAAAAAGA 1329
Qy    816  GlnIleGlyLeuTyrArgAspThrValArgAspThrArgLeuPheArgGlyIleLeuAspGly 835
             :::||||
Db   1330  AGAGGCGAGAAACTAGACAAAGTTTGGCTTTGGAACTCCTTTGAACAAATAACAAAAGGG 1389
Qy    836  LeuAlaTyrIleHisGluHisGlyMetIleHisArgAspLeuLysLysThrLeuAsnIlePhe---- 855
             :::
Db   1390  GTGATTATATACATTCAAAAAAAATTAATTCATAGAGATCTTAAGCACCAAGTAATATATTC 1449
Qy    856  LeuAspSerSerAspHisValLysValIleGlyPheGlyLeuAlaThrAspHisLeuAla 875
             :::||||
Db   1450  TTAGTAGATACAAAACAAGTAAAGATTGGAGACTTTGGACTTGTAACATCT--------- 1500
Qy    876  PheSerAlaAspSerLysLysSerGlnInAspAspLeuLeuLysSerAspProSer 895
             ||||:::
Db   1501  ------CTGAAAAATGAT------ 1512
Qy    896  GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValIleGlnSer 915
             ||||
Db   1513  GGAAAGGCGGACAAGGAGTAGGGGGACTTTGCGACACATACAGACAGATTTCTTCG 1572
Qy    916  ThrLysSerAlaTyrAsnGlnLysValAspPheLeuSerPheLeuGlyIleIlePhePheGlu 935
             |||:::|:
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Qy  722 gPheProAlaThrGlyProGlySerSerAspAspGluAspAspGluAspGluHisGl 742
                                 :::
Db 1832 GATA----------------------AGCCTGTCCACAGCAGAGGGCATCAAGGGC 1876

Qy  742 yGlyValPheSer--------------------GlnSerPheLeuProAlaSerAspSerGluse 757
              |||||                         :::
Db 1877 TGGCTAGGAAGATAGGAAATGCAATGAGGAGAGTCTGTTGCTGTATCCCATCCAAAGAG 1936

Qy  757 rAspIlePheAspAsnGluAsnSerLysSerGlnAsnGlnAsnGlnAspGluAspCy 777
              ||                              :::
Db 1937 ACATTCCACCTGGGCACAGAGAAGAGTCTGCCCAAAAATTTAAGACACAGAA--------- 1988

Qy  777 sAsnGluLysAsnGlyCysHisGluserGlu--------ProSerValThr-ThrG 793
              ||||                  ||||||::::
Db 1989 ------------GGATGCAGGAGAATGAGCATCCAGCATGGCCCAGCCTTTCAGACCG 2035

Qy  793 luAlaValHisTyrTyrLeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspT 813
                       :::        ---ArgAspThrValArgLeuTrpArgLeuPheArgG
Db 2036 AAGGC------AAGCTCACCTGATCCTGGACTTCCTGCGGGGAGGTGACCTCTTCACCA 2089

Qy  813 hrIleAspIleGlyLeuTyr-----------ArgAspThrValArgLeuTrpArgLeuPheArgG 831
                    :::    :::  :::::::::::   ||||||
Db 2090 GGCTTCCAAAGAGGTGATGTTCACGGAGGAGATGTCAAGTTCTAC----CTGGCTG 2143

Qy  831 luIleLeuAspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysP 851
              ||||||                :::::::::
Db 2144 AGTCGGCCTGGCTCTAGACCACCTCCATGGCCTGGGGATCATCTACAGGGATCTGAAGC 2203

Qy  851 roValAsnIlePheLeuAspSerAspHisValLysIleGlyValAspPPheGlyLeu----- 869
                :::        :::::::
Db 2204 CAGAGAATATCCCTCCTGGATGAAGAGGGACATATTAAGATCACAGATTTTGGCTTGAGCA 2263

Qy  870 --------AlaThrAspHis---------LeuAlaPheSerAlaAspSerLysGlnAspAspGlnT 886
                    |||::::          ||||||::::
Db 2264 AGGAGGCCACCGACCATGACAAGAGAGCCTATTCA 2298

Qy  886 hrGlyAspLeuIleLysSerAspArgProSerGlyHisLeuThrGlyMetValGlyThrAlaL 906
                :::::::                        ||||||
Db 2299 TTTTGTGGGACTATTG 2314

Qy  906 euTyrValSerProGluVal----------GlnGlySerThrLysSerAlaTyrAsnGlnLnL 923
              :::::::          :::|||||||
Db 2315 AATACATGGCGCCGAGGTGGTGAACCGGCTGGACACACAGAGTGCC-------- 2364

Qy  923 ysValAspLeuPheSerLeuGlyIleIlePhePheGluMetSerTyrHisProMetValT 943
                      :::::::          |||||||:::
Db 2365 ----GACTGGTGGTCCTTCGGTGTGCTCATGTTCGAGATGCT-CAC------ 2405

Qy  943 hrAlaSerGluArgIlePheValLeuAsnGlnLeuArgAspProThrSerProLysSerPheP 963
                                        :::::::|||||||
Db 2406 -------------------AGGGTCCCTGCCATTCCAGGGGGAAG 2430

Qy  963 roGluAspPheAspAspGlyGluHisAlaLysGlnLys----------SerValIleSerT 980
                    :::                        :::|||||||
Db 2431 GACAGGAAGAAACAATGGCCGCATCCTCAAAGCAAAGCTGGGTATGCCTTAGTTCCTC 2490

Qy  980 rpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeuLeuLys---------- 997
                      :::::::          ||||||
Db 2491 AGTGCGGAGGCTGCTCAGGCGCCCTTTTCAGCGGACACCCCGCACCGGCTA-------- 2550

Qy  998 --------SerGluLeuLeuProProProGlnMetGluGluSerGluLeuHisGlu---V 1014
                    :::::::                        :::|||||||
Db 2551 GGTAAGGGTCCCT-GTGACACCCCCACCCCAG---------GAATGCAATGAGGGCTG 2597

Qy 1014 aLeuHisHisThrLeuThrAsnValAspGly 1024
              ||||||
Db 2598 CCCTCTAGACCCCCCCCTTAGGAATGTGAGAGGC 2629
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RESULT 14
US-09-554-726A-20
; Sequence 20, Application US/09554726A
; Patent No. 6642369

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Db  839 CCATTATTCAAGCAGCTCTTAAGTGCTATGAACTACTGCCCAACCAGGTATAGTTCAC 898

Qy  424 LysValValLeuSerAlaSerAsnValLeuVaLaAspAlaGluGlyThrLysValLysIleThrAsp 443
              :::   |||        ::::::::
Db  899 AGGGACCTGACACCTGACAATATTATGTAGAAAAAGATGGAAAGTGAAGATCATTGAT 958

Qy  444 TyrSerIleSerLysArgLeuAlaAsp------------------IleCysLysGluAsp 457
              :::                              :::|||
Db  959 TTTGGACTTCGGCACCCAAGAGAGCCAGGCAAAACCAACTATTCTGTGAGATTAC 1018

Qy  458 ValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLys 477
              |||                        :::---AGACCCTATGATATG---CGC 1066
Db 1019 CCATTTTAGTACTCCTGAGGTGCTCTTTAAC------------------AGACCCTATGATATG---CGC 1066

Qy  478 LysGlyAspValTrpArgLeuGlyLeuLeuLeuSerLeuSerGlnGly------------- 494
              |||                        ::::::::
Db 1067 AAGATCGATGTGTGGGGTCTTGGAGTTCTGCTGTATTTATGTCTGTAACTGAAAGATTCTG 1126

Qy  495 ------------------GlnGluCysGlyValGlu 499
                                  :::|||
Db 1127 TTTGATACTGCCAGCTGAGAAAAGCTCGCGAAAAGCAAATTGTTGCAGAAAAGTGT---- 1180

Qy  500 TyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLysLysCys 519
              :::                        :::|||
Db 1181 --------TCTGTTCCCTGTAGACTGTCAGTAGAGCTCCAAGACCTGATTAGACTTTTA 1231

Qy  520 ValCysLeuAspAspLysProGlnLnLeuLysHisSerPheIle 539
              :::                        :::||| :::::::
Db 1232 ATGACGGACACTCCCGAACTTAGGCCCACTGGTTGCTGAAGTTATGGTGCATCCCTGGGTC 1291

Qy  540 AsnProGlnProLysMetProLeuValGluGlnSerProGluGlnAspSerGlyGly---Gln 558
              :::                        :::|||
Db 1292 ACA------------------GAAGGCTCAGGGGTGTTACCA 1315

Qy  559 AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAla------------ 574
              :::                        |||
Db 1316 GATCCTGTGAAGAACATATACCCCCTCAAGCCAGACCCTGCGATTGCAAAAGCAATGGGA 1375

Qy  575 PhePhe------------------SerGluThrGlnArgGlnPheSerArg 585
              |||                        :::
Db 1376 TTTATCGGGTTCCAAGCTCAAGACATTGAAGATTCGTTATGTCAGAGAAAATTCAACGAA 1435

Qy  586 TyrPheIleGluProGluLeuGlnLeuLeuGlyLysLysGlyLysGlyGlyAlaPheGlyAlaValIle 605
              :::                        :::
Db 1436 ACCATGGCATCTTAT------------------TGTCTACTG 1459

Qy  606 LysValGlnAsnLysLeuAspGlyCysCysTyrAlaValLysArgIleProIleAsnPro 625
              |||                        :::
Db 1460 AAAAAACAG--ATTCTTAAGGAATGTGACAGGCAATCCGGGCTCAGCCCATGAATCCA 1516

Qy  626 AlaSerArgGln------------------PheArgArg 632
              |||                        :::
Db 1517 TCTGTGACCCCACTCTCTTCCCTGTTGATGCCTCCTACTTCCATCTCGGACTTCGGAGG 1576

Qy  633 IleLeuLysGlyValThrLeuLeuSerArgLeuHisGluAsnIleValArgTyrTyr 652
              :::                        |||
Db 1577 ACAGGAAGGACTGAACCCCACAGGTCTCAGATTATCTGACAATAAGGAAGTGCCTGTTCTGTGGC 1636

Qy  653 AsnAlaTrpIleGluArgHisGluArgPro---AlaGlyProGlyThrProProProAsp 671
              :::                        |||
Db 1637 AATAGTACTAGTAGAAAGAGAGAAGAAGTTTCAGTGGGCCGGGT-------------------- 1681

Qy  672 SerGlyProLeuAlaLysAspAspAlaArgAlaAlaArgGlyGlnProAlaSerAspThrAsp 691
              :::                        :::|||
Db 1682 ------------------GTTCTCAGCAGGCCGATTAACACAACACCCC 1711

Qy  692 GlyLeuAspArgSerValGluAlaAla------AlaProProIleLeuSer---------- 706
              :::                        :::
Db 1712 ACAATGGACCAAACACACACCCGTACTTGGAGTGGTCCCATTTACTCAAATGTTTGC 1771

Qy  707 ------------------SerSerValGluTrpSerGlyValArgSerAlaSerAla-Ar 722
                                  :::
Db 1772 ACAATCCATCCAAACAGCATCAATGGAGTACAGAGAGCCACATCCAGTACCTCAGCAGAG 1831
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GENERAL INFORMATION:
APPLICANT: HERRMANN, Bernhard
APPLICANT: KOSCHORZ, Birgit
APPLICANT: KISPERT, Andreas
TITLE OF INVENTION: NUCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATION
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 258.0009 0101
CURRENT APPLICATION NUMBER: US/09/554,726A
CURRENT FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: PCT/EP 98/07395
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: EP 98 10 3596.7
PRIOR FILING DATE: 1998-03-02
PRIOR APPLICATION NUMBER: EP 97 12 0190.0
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 2827
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (2002)..(2481)
OTHER INFORMATION:
US-09-554-726A-20

Alignment Scores:
Pred. No.:   2827
Score: 6.06e-26   Length: 2827
              358.00   Matches: 185
Percent Similarity: 39.90%   Conservative: 123
Best Local Similarity: 23.96% Mismatches: 254
Query Match: 4.19%   Indels: 212
DB: 4   Gaps: 35

US-09-515-806A-2 (1-1649) x US-09-554-726A-20 (1-2827)

Qy   345 ThrGluPheAsnSerLeuValLysLeuSerHisProAsnValValArgTyrLeu--Ala 363
           ::|||| ||:||||: ||||
Db   674 TCTGAGGCAGAGTTACTGAGTGATGACCGATCATCCGAATATCATCTCTCCTTCAAGTC 733

Qy   364 MetAsnLeuLysGluGlnGlnAspAspSerIleValValAspIleLeuValGluHisIleSer 383
           ::: ||:||||:: || ::|||||:||:|||
Db   734 ATTGAGACCAAGAGAAA------------GTATACCTCATTATGGAGTTGTGCGAG 778

Qy   384 GlyValSerLeuAlaAlaHisLeuSerGlyProIleProValHisGlnLeuArg 403
           |||::| |:: |||||||||:::
Db   779 GGTAAATCACTTTACCCAACACATCCAAAATGCTGGCTACCTGCAGGAGGAGCACGC 838

Qy   404 ArgTyrThrAlaGlnLeuLeuSerGlyLeuAspTyrLeuAspThrGluAsnSerValValHis 423
           |||||| |:::|||:|||::   ::|||||
Db   839 CCATTATTCAAGCAGTCTCTTAAGTGCTATGAAGTCACTGCCACACCCAGGGTATAGTTCAC 898

Qy   424 LysValLeuSerAlaSerAsnValLeuValAspAlaGluGlyThrValLysIleThrAsp 443
           :||:||| |||:||||||||::||:
Db   899 AGGGACCTGACACCTGACACAATATTATGGTGAGAAAAAGATGGAAAGTGAAGATCATTGAT 958

Qy   444 TyrSerIleSerLysArgLeuAlaAsp-------------IleCysLysGluAsp 457
           ||: |||
Db   959 TTTGGACTCGGCACCCAAGAGAAGGCCAGGGCAAAACCAACTTATTCTGTGAGATTTAC 1018

Qy   458 ValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLys 477
           ::: |||:||:
Db   1019 CCATTTAGTACTCCTGGAGGTGCTCTTTAAC-----AGACCCTATGATATG---CGC 1066

Qy   478 LysGlyValAspValTrpArgLeuGlyLeuGlyLeuLeuLeuLeuSerLeuSerGlyGly 494
           ||:   ::|
Db   1067 AAGATCGATGTGTGGGGGTCTTGGAGTTGTGCTGTATTTATGGTAACTGGAAAGATTCTG 1126

Qy   495 GlnGluCysGlyGlu 499
                          :::|||||
Db   1127 TTTGATACTGCCAGCTGTAGAAAAAGTCTGCGAAAGCAAATTGTTGCAGAAAGTGT------ 1180

Qy   500 TyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeuLysLysCys 519
           :::||| |||
Db   1181 ------------TCTGTTCCCTGTAGAGACTGTCAGTAGAGCCTCAAGACCTGATTAGACTTTTA 1231

Qy   520 ValCysLeuAspAspLysGluTrpSerProGlnGlnLeuLeuLeuHisSerPheIle 539
           ::| ||
Db   1232 ATGACGGACATCCCGAACTTAGGCCCACTGTGCTGAGTTATGGTGCATCCCTGGGTC 1291

Qy   540 AsnProGlnProLysMetProLeuValGluGlnSerProLeuAspSerGlyGly--Gln 558
           ||| :::|||
Db   1292 ACA------------------------GAAGGCTCAGGGGTGTTACCA 1315

Qy   559 AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAla---------- 574
           |||:||| |||:
Db   1316 GATCCTTGTGAGAACATATCCCCTCAAGCCAGACCCTGCAAAAGCAATGGGA 1375

Qy   575 -----SerGluThrGlnArgGlnPheSerArg 585
                :::|
Db   1376 TTTATCGGGTTCCAAGCTCAAGACATTGAGAATTCGTTATGTCAGAGAAAATTCAACGAA 1435

Qy   586 TyrPheIleGluPheGluGlnLeuGlnLeuGlyLysGlyLysAlaPheGlyAlaValIle 605
                              :::
Db   1436 ACCATGGCATCTTAT------------------------TGTCTACTG 1459

Qy   606 LysValGlnAsnLysLeuAspGlyCysCysTyrAlaValAlaLysArgIleProIleAsnPro 625
                                     ||:||:|||||||:
Db   1460 AAAAAACAG---ATTCTTAAGGAATGTGACAGGCCAATCCGGGCTCAGCCCATGAATCCA 1516

Qy   626 AlaSerArgGln------------------------------------PheArgArg 632
           :::
Db   1517 TCTGTGACCCCACTCTCCTTCCCTTGTGATGGTCCTACTTTCCATCTCGGACTTCGGAGG 1576

Qy   633 IleLysGlyGlyValThrLeuSerArgLeuHisLeuSerArgLeuHisGluAsnIleeValArgTyrTyr 652
           :::
Db   1577 ACAGAGACTGAACCCACCAGGTCTCAGATTATCTGACAATAAGGAAGTGCCTGTCGTGGC 1636

Qy   653 AsnAlaTrpIleGluArgHisGluArgPro---AlaGlyProGlyThrProProProAsp 671
           :::|||||:   ::|||||||
Db   1637 AATAGTACTAGTAAGAAAAAGAGAGAAGTTTCAGTGGGCCCGGT 1681

Qy   672 SerGlyProLeuAlaLysAspAspAspAspSerAspArgAlaAlaArgGlyGlnProAlaSerAspThrAsp 691
                                                          :::
Db   1682 ---------------------------GTTCTCAGCAGGCGATTAACACAACACCCC 1711

Qy   692 GlyLeuAspSerValGluAlaAla------AlaProProProIleLeuSer- 706
           ::: |||
Db   1712 ACAATGGACCCAAACACACCACCCTACTTGGAGTGGTCCCTGCATTACTCAAAATGTTTGC 1771

Qy   707 ------SerSerValGluTrpSerThrSerGlyGluArgSerAlaSerAla--Ar 722
                                     ::|||||
Db   1772 ACAATCCATCCAAACAGCATCAATCAATGAGTACGAAGGCCACACTCAGTACCTCAGCAGAG 1831

Qy   722 gPheProAlaThrGlyProGlySerSerAspAspSerAspAspAspGlnGlyHisGlyGlnHisGl 742
           |||
Db   1832 GATA----------------------------------AGCCTGTCCCACAGCAGAGGCTGGCCCAGGGCATCAAGGGC 1876

Qy   742 yGlyValPheSer--------GlnSerPheLeuProAlaSerSerGluSe 757
           :::
Db   1877 TGGACTAGGAAGATAGGAAATGCAATGAGGAAGTCTCGTTGCTGTATCCCATCCAAAGAG 1936

Qy   757 rAspIleIlePheAspAspAsnGluAspLysAsnSerLysSerGlnAsnGlnGluAspCy 777
           ::: ||||:
Db   1937 ACATCCCACCTGGGCGCAGAGAAGAGTCTGCCAAAAATTAAGACACAGGAA----- 1988

Qy   777 sAsnGluLysAsnGlyCysHisLysSerGlu--------ProSerValThr-ThrG 793
                            ||||:||:
Db   1989 ----------GGATGTCAGGAGAATGAGCATCCAGCATGCGCCAGCCTTTCAGACCG 2035

Qy   793 luAlaValHisTyrLeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspT 813
           :::   ::|||
Db   2036 AAGGC-------AAGCTCTACCTGACTCCTGCGGGGGAGGTGACCTCTTCACCA 2089

Qy   813 hrIleAspGlnGlyLeuTyr-------ArgAspThrValArgLeuTrpValArgLeuPheArgG 831
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DB:

US-09-515-806A-2 (1-1649) x US-09-803-671B-1 (1-4307)

Gaps: 21

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RESULT 15
US-09-803-671B-1
; Sequence 1, Application US/09803671B
; Patent No. 6582946
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001161
; CURRENT APPLICATION NUMBER: US/09/803,671B
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 4307
;   TYPE: DNA
;   ORGANISM: Human
US-09-803-671B-1
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Alignment Scores:

Pred. No.:		Length:	4307
Score:	8.6e-22	Matches:	128
	321.00	Conservative:	100
Percent Similarity:	38.13%	Mismatches:	210
Best Local Similarity:	21.40%	Indels:	160
Query Match:	3.76%		

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b   3397 AAACAAATACTTCAAGGTGTTGCTTATCTCCATGAGAACTGTGTGGTACATCGCGATATC 3456
             ||||::||      |||::||           |||          ||||||||||  :::
y    427 SerAlaSerAsnValLeuValAspAlaGluGlyThrValLysIleThrAspTyrSerIle 446
             :::||||||||      :::|||||||::
b   3457 AAAGGAAATAATGTTATGCTCATGCCAACTGGAATAATAAAGCTGATTGACTTGGCTGT 3516

y    447 SerLysArgLeuAla------------------AspIleCysLysGluAsp 457
             :::::|||||||||                  |||:::  |||
b   3517 GCCAGGGGTTTGGCCTGGGCAGGTTTAAATGGCACCCACCAGTGACATGCTTAAG------ 3570

y    458 ValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyr------------- 473
             |||             ::||       |||||
b   3571 -------------------------TCCATGCATGGGACTCCATATTGGATGGCCCCA 3603

ly   474 ------------LysThrGlyLysGlyValAspValTrpArgLeuGlyLeuLeu 487
             :::||||:::||   |||:::||      :::|||
yb  3604 GAAGTCATCAATGAGTCTGGCTATGGACGGAAATCAGATATCTGGAGCATTGGTTGTTACT 3663

ly   488 LeuLeuSerLeuSerGlnGlyGlu----------------------------- 496
             ::         :::|:::|||
yb  3664 GTGTTTGAGATGGCTACAGGGAAGCCTCCACTGGCTTCCATGGACAGGATGGCCGCCATG 3723

ly   497 -----CysGlyGluTyrProValThrIleProSerAspLeuProAlaAspPheGln-- 513
             :::          ||||||
yb  3724 TTTTACATCGGAGCACCGAGGGGTGATGCCT--CCTTTACCAGACCACTTCTCAGAA 3780

ly   514 -------AspPheLeuLysCysValCysLeuAspAspLysGluArgTrpSerPro 530
             ||||:::::|      |||:::         |||
Db  3781 AATGCAGCAGACTTGTGCGCATGTCCTGACCAGGACCATGAGCGACCTTCTGCT 3840

Qy   531 GlnGlnLeuLeuLysHisSerPheIleAsnProGlnProLysProLeuValGluGln 550
             ||||||||||   ||||||           :::
Db  3841 CTCCAGTCCCTGAAGCACTCCTTCTTCTTGGAGAGAAGTCACTGAATA------- 3885

Qy   551 SerProGluAspSerGlyGlyGlyValGlnAspTyrValGluThrVal-----IleProSerAsn 568
             ||:::::|||      :::|||
Db  3886 -------------------TACATCAAGACTTTCTTCCCAGTTCCACTGCAG 3918

Qy   569 ArgLeuProSerAlaAlaPhePheSerGluThrGlnArgGlnPheSerArgTyrPheIle 588
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Db  3919 ATGCTCCCTTGCTTAATTGTGGGGAATGAT------------------------- 3948

Qy   589 GluPheGluGluLeuGlnLeuLeuGlyLysGlyAlaPheGlyAlaValIleLysValGln 608
             :::   |||   |||   :::|||:::||||||:::|||
Db  3949 -------GGCTAAGGGATCTTTGTTTCCCCACTGAAAATTCAG 3984

Qy   609 AsnLys-----------LeuAspGlyCysCysTyr 616
             :::   :::
Db  3985 TCTAACCCAGTTTAAGCAGATCCTATGGAGTCATTAACTGAAAGTTGCAGTTAC 4038

Search completed: March 22, 2004, 01:51:23
Job time : 247 secs
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